

=> d his

(FILE 'HOME' ENTERED AT 09:55:53 ON 29 DEC 2003)
SET COST OFF

FILE 'HCAPLUS' ENTERED AT 09:56:12 ON 29 DEC 2003
L1 4 S (US20030087820 OR US20030036504)/PN OR (US2001-889331# OR US9
E GEDULIN B/AU
L2 22 S E3,E6,E7
E YOUNG A/AU
L3 111 S E3,E4
L4 103 S E141,E142
L5 3 S E159
E AMYLIN/PA,CS
L6 143 S E3-E29
L7 16 S L1-L6 AND EXENDIN?

FILE 'REGISTRY' ENTERED AT 10:00:10 ON 29 DEC 2003
E EXENDIN

L8 239 S E3

FILE 'HCAPLUS' ENTERED AT 10:00:20 ON 29 DEC 2003

L9 231 S L8
L10 282 S EXENDIN?
L11 16 S L1-L6 AND L9,L10
L12 16 S L7,L11
L13 9 S L12 AND P/DT
L14 9 S L1,L13

FILE 'REGISTRY' ENTERED AT 10:01:52 ON 29 DEC 2003

L15 140 S [HRT][SGAT][DE]GT[FYA][TS][TS][DE][LIVMG'UND']SKQ[LIVMG'UND']
L16 124 S L15 AND 39-40/SQL
L17 16 S L15 NOT L16
SAV L16 LIU889A/A
L18 42 S [SGAT][DE]GT[FYA][TS][TS][DE][LIVMG'UND']SKQ[LIVMG'UND']EEEEAV
L19 10 S L18 NOT L15
L20 0 S L19 AND 38-40/SQL
E HSDGTFTSDLSKQMEEEAVRLFIEWLKNGGPSSGAPPPS/SQEP
L21 11 S E3
E HGEFTFTSDLSKQMEEEAVRLFIEWLKNGGPSSGAPPPS/SQEP
L22 21 S E3
L23 92 S L16 NOT L21,L22
SAV L23 LIU889B/A

FILE 'HCAOLD' ENTERED AT 10:14:05 ON 29 DEC 2003
L24 0 S L23

FILE 'HCAPLUS' ENTERED AT 10:14:09 ON 29 DEC 2003

L25 13 S L23
L26 7 S L25 AND L1-L6
L27 10 S L25,L26 AND (PY<=1999 OR PRY<=1999 OR AY<=1999)
L28 3 S L25,L26 NOT L27
L29 1 S L26 AND L28
L30 11 S L27,L29

FILE 'USPATFULL, USPAT2' ENTERED AT 10:16:37 ON 29 DEC 2003
L31 11 S L23

=> fil reg

FILE 'REGISTRY' ENTERED AT 10:17:16 ON 29 DEC 2003
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liu - 09 / 889331

Property values tagged with IC are from the ZIC/VINITI data file provided by InfoChem.

STRUCTURE FILE UPDATES: 28 DEC 2003 HIGHEST RN 631841-90-2
 DICTIONARY FILE UPDATES: 28 DEC 2003 HIGHEST RN 631841-90-2

TSCA INFORMATION NOW CURRENT THROUGH JULY 14, 2003

Please note that search-term pricing does apply when conducting SmartSELECT searches.

Crossover limits have been increased. See HELP CROSSOVER for details.

Experimental and calculated property data are now available. For more information enter HELP PROP at an arrow prompt in the file or refer to the file summary sheet on the web at:
<http://www.cas.org/ONLINE/DBSS/registryss.html>

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=> d sta que l16
L15      140 SEA FILE=REGISTRY ABB=ON PLU=ON [HRT][SGAT][DE]GT[FYA][TS][TS]
        ] [DE][LIVMG'UND']SKQ[LIVMG'UND']EEEEAVRL[FYA][IVLMG'UND'] [DE][WF
        YA]LKNKG.SSGA...[STY]/SQSP
L16      124 SEA FILE=REGISTRY ABB=ON PLU=ON L15 AND 39-40/SQL
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=> d sta que l18
L18      42 SEA FILE=REGISTRY ABB=ON PLU=ON [SGAT][DE]GT[FYA][TS][TS][DE]
        [LIVMG'UND']SKQ[LIVMG'UND']EEEEAVRL[FYA][IVLMG'UND'] [DE][WFYA]LK
        .{0,1}[KN]GG.SSGA...../SQSP
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=> fil hcaplus
FILE 'HCAPLUS' ENTERED AT 10:17:39 ON 29 DEC 2003
USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.
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FILE COVERS 1907 - 29 Dec 2003 VOL 140 ISS 1
 FILE LAST UPDATED: 28 Dec 2003 (20031228/ED)

This file contains CAS Registry Numbers for easy and accurate substance identification.

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=> d all tot 130
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L30 ANSWER 1 OF 11 HCAPLUS COPYRIGHT 2003 ACS on STN
AN 2003:355827 HCAPLUS
DN 138:374157
ED Entered STN: 09 May 2003
TI Novel exendin agonist formulations and methods of administration ther
```

liu - 09 / 889331

IN Young, Andrew A.; Kolterman, Orville G.
 PA USA
 SO U.S. Pat. Appl. Publ., 104 pp., Cont.-in-part of U.S. Ser. No. 889,330.
 CODEN: USXXCO
 DT Patent
 LA English
 IC ICM A61K038-17
 NCL 514012000
 CC 63-6 (Pharmaceuticals)
 FAN.CNT 4

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2003087820	A1	20030508	US 2002-157224	20020528 <--
WO 2000041546	A2	20000720	WO 2000-US902	20000114 <--
W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, VZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
WO 2003099314	A1	20031204	WO 2003-US16699	20030528
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, VZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
PRAI US 1999-116380P	P	19990114 <--		
US 2000-175365P	P	20000110		
WO 2000-US902	W	20000114		
US 2001-889330	A2	20011227		
US 2002-157224	A	20020528		
AB			Novel exendin and exendin agonist compound formulations and dosages and methods of administration thereof are provided. These comps. and methods are useful in treating diabetes and conditions that would be benefited by lowering plasma glucose or delaying and/or slowing gastric emptying or inhibiting food intake.	
ST			exendin agonist formulation antidiabetic	
IT			Antidiabetic agents	
			Cardiovascular system, disease	
			Diabetes mellitus	
			Human	
			Protein sequences	
			(exendin agonist formulations and methods of administration thereof)	
IT			Drug delivery systems	
			(intratracheal; exendin agonist formulations and methods of administration thereof)	
IT			Drug delivery systems	
			(oral; exendin agonist formulations and methods of administration thereof)	
IT			Drug delivery systems	
			(parenterals; exendin agonist formulations and methods of administration thereof)	
IT			Drug delivery systems	
			(sublingual; exendin agonist formulations and methods of administration thereof)	

thereof)

IT Drug delivery systems
(sustained-release; exendin agonist formulations and methods of administration thereof)

IT Drug delivery systems
(transdermal; exendin agonist formulations and methods of administration thereof)

IT Drug delivery systems
(transmucosal; exendin agonist formulations and methods of administration thereof)

IT 522007-52-9 522007-56-3 522007-58-5 522007-60-9
RL: PRP (Properties)
(Unclaimed; novel exendin agonist formulations and methods of administration thereof)

IT 213190-65-9, Exendin
RL: BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(agonists; exendin agonist formulations and methods of administration thereof)

IT 89750-14-1, Glucagon-like peptide I 141732-76-5, Exendin 4
RL: BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(exendin agonist formulations and methods of administration thereof)

IT 521986-08-3
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(unclaimed protein sequence; exendin agonist formulations and methods of administration thereof)

IT 522007-04-1 522007-05-2 522007-06-3 522007-07-4 522007-08-5
522007-09-6 522007-10-9 522007-11-0
522007-12-1 522007-13-2 522007-14-3
522007-15-4 522007-16-5 522007-17-6
522007-18-7 522007-19-8 522007-20-1 522007-21-2
522007-22-3 522007-23-4 522007-24-5 522007-25-6
522007-26-7 522007-27-8 522007-28-9 522007-29-0
522007-30-3 522007-31-4 522007-32-5
522007-33-6 522007-34-7 522007-35-8 522007-36-9 522007-37-0
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522007-43-8 522007-44-9 522007-45-0 522007-46-1 522007-47-2
522007-48-3 522007-49-4 522007-50-7 522007-51-8 522007-53-0
522007-54-1 522007-55-2 522007-57-4 522007-59-6 522007-61-0
522007-62-1 522007-63-2 522007-64-3 522007-65-4 522007-66-5
522007-67-6 522007-68-7 522007-69-8 522007-70-1 522007-71-2
522007-72-3 522007-73-4 522007-74-5 522007-75-6 522007-76-7
522007-77-8 522007-78-9 522007-79-0 522007-80-3 522007-81-4
RL: PRP (Properties)
(unclaimed protein sequence; novel exendin agonist formulations and methods of administration thereof)

IT 165338-05-6, 1-31-Exendin 4 (Heloderma suspectum) 210712-28-0,
1-30-Exendin 4 (Heloderma suspectum) 238091-56-0 238091-57-1
238091-58-2 238091-59-3 238091-60-6 238091-61-7 238091-62-8
238091-63-9 238091-64-0 238091-65-1 238091-66-2 238091-67-3
238091-68-4 238091-69-5 238091-70-8 238091-71-9 238091-72-0
238091-73-1 238091-74-2 238091-75-3 238091-76-4 238091-77-5
238091-78-6 238091-79-7 238091-80-0 238091-81-1 238091-82-2
238091-83-3 238091-84-4 238091-86-6 238091-87-7 238091-88-8
238091-92-4 238091-93-5 238091-94-6 351208-37-2 351208-40-7
351208-41-8 351208-42-9 351208-43-0 351208-44-1 351208-45-2
351208-46-3 351208-47-4 351208-48-5 351208-49-6 351208-50-9
351208-53-2 351208-54-3 351208-55-4 351208-56-5 351208-57-6
351208-58-7 351208-59-8 351208-60-1 351208-61-2 351208-62-3
351208-65-6 351208-66-7 351208-67-8 351208-68-9 351208-69-0
351208-70-3 351208-72-5 351208-74-7 351208-78-1 351208-79-2

351208-80-5 351208-81-6 351208-82-7 351208-83-8 351208-84-9
 351208-85-0 351208-86-1 351208-88-3 351208-89-4 351208-90-7
 351208-93-0 351208-94-1 351208-97-4 351208-98-5 351208-99-6
 351209-00-2 351209-01-3 351209-02-4 351209-03-5 351209-04-6
 351209-05-7 351209-06-8 351209-07-9 351209-08-0 351209-09-1
 351209-10-4 351209-11-5 351209-12-6 521913-27-9 521913-28-0
 521913-29-1 521913-30-4

RL: PRP (Properties)

(unclaimed sequence; novel exendin agonist formulations and methods of administration thereof)

L30 ANSWER 2 OF 11 HCAPLUS COPYRIGHT 2003 ACS on STN

AN 2001:525943 HCAPLUS

DN 135:132445

ED Entered STN: 20 Jul 2001

TI Use of exendins and agonists thereof for modulation of triglyceride levels and treatment of dyslipidemia

IN Kolterman, Orville Gene; Young, Andrew A.

PA Amylin Pharmaceuticals, Inc., USA

SO PCT Int. Appl., 161 pp.

CODEN: PIXXD2

DT Patent

LA English

IC ICM A61K038-22

ICS A61P003-06; A61K038-22; A61K031-20; A61K038-22; A61K031-22;

A61K038-22; A61K031-365; A61K038-22; A61K031-40

CC 1-10 (Pharmacology)

FAN.CNT 4

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE	
PI	WO 2001051078	A1	20010719	WO 2001-US719	20010109	
	W:			AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM		
	RW:			GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG		
	EP 1246638	A1	20021009	EP 2001-900978	20010109	
	R:			AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR		
	US 2003036504	A1	20030220	US 2001-756690	20010109 <--	
	JP 2003519667	T2	20030624	JP 2001-551501	20010109	
PRAI	US 2000-175365P	P	20000110			
	WO 2001-US719	W	20010109			
AB	Methods for modulating the levels of plasma triglyceride and other lipids in a subject comprise administration of an effective amount of an exendin or exendin agonist, alone or in conjunction with other compds. or compns. that lower blood triglyceride and/or other lipid levels.					
ST	hypolipidemic triglyceride dyslipidemia treatment exendin					
IT	Antidiabetic agents					
	Heart, disease					
	Hypolipemic agents					
	(exendins and agonists for modulation of triglyceride levels and treatment of dyslipidemia)					
IT	Glycerides, biological studies					
	RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)					
	(exendins and agonists for modulation of triglyceride levels and treatment of dyslipidemia)					
IT	Drug delivery systems					

(injections, s.c.; exendins and agonists for modulation of triglyceride levels and treatment of dyslipidemia)

IT Drug delivery systems
(injections; exendins and agonists for modulation of triglyceride levels and treatment of dyslipidemia)

IT Diabetes mellitus
(non-insulin-dependent; exendins and agonists for modulation of triglyceride levels and treatment of dyslipidemia)

IT 210712-29-1 210712-30-4 210712-33-7 210712-34-8 210712-35-9
 210712-36-0 210712-37-1 210712-38-2 210712-39-3 210712-40-6
 210712-41-7 210712-42-8 210712-43-9 210712-44-0 210712-45-1
 210712-46-2 210712-47-3 210712-48-4 210712-49-5 210712-50-8
 210712-51-9 210712-52-0 210712-53-1 210712-69-9 210712-70-2
 210712-71-3 210712-72-4 285554-80-5 285554-82-7 285554-84-9
 350586-34-4 350586-35-5 351340-03-9 351340-08-4 351340-10-8
 RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
 (exendins and agonists for modulation of triglyceride levels and treatment of dyslipidemia)

IT 130391-54-7, Exendin 3 141732-76-5, Exendin 4 213190-65-9, Exendin 213190-65-9D, Exendin, analogs and derivs.
 RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
 (exendins and agonists for modulation of triglyceride levels and treatment of dyslipidemia)

IT 50-99-7, D-Glucose, biological studies 9007-92-5, Glucagon, biological studies
 RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
 (exendins and agonists for modulation of triglyceride levels and treatment of dyslipidemia)

IT 203743-40-2 238410-89-4 238410-90-7 238411-00-2 238411-01-3
 238411-02-4 238411-03-5 238411-04-6 238411-05-7 238411-06-8
 238411-07-9 238411-08-0 238411-10-4 238748-48-6 306277-48-5
 351350-30-6 351350-32-8 351350-38-4
 351350-40-8 351350-43-1 351350-44-2
 351350-45-3 351350-47-5 351350-91-9
 351351-05-8 351351-08-1 351351-09-2 351351-14-9
 351351-26-3 351351-27-4 351351-28-5 351351-29-6 351351-30-9
 351351-31-0 351351-32-1 351351-33-2 351351-46-7 351351-47-8
 351376-16-4 351376-17-5 351376-18-6
 351376-19-7 351376-20-0 351376-22-2
 351376-23-3 351376-24-4 351376-25-5
 351376-49-3 351376-51-7 351376-52-8 351376-66-4 351376-82-4
 RL: PRP (Properties)
 (unclaimed protein sequence; use of exendins and agonists thereof for modulation of triglyceride levels and treatment of dyslipidemia)

IT 165338-05-6, 1-31-Exendin 4 (Heloderma suspectum) 210712-28-0,
 1-30-Exendin 4 (Heloderma suspectum) 238091-60-6 238091-78-6
 238091-79-7 238091-80-0 238091-81-1 238091-82-2 238091-83-3
 238091-84-4 238091-86-6 238091-87-7 238091-88-8 238091-92-4
 238091-93-5 238091-94-6 351208-37-2 351208-38-3 351208-39-4
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 351208-83-8 351208-84-9 351208-85-0 351208-86-1 351208-88-3

351208-89-4 351208-90-7 351208-91-8 351208-92-9 351208-93-0
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 351208-99-6 351209-00-2 351209-01-3 351209-02-4 351209-03-5
 351209-04-6 351209-05-7 351209-06-8 351209-07-9 351209-08-0
 351209-09-1 351209-10-4 351209-11-5 351209-12-6 351351-15-0

RL: PRP (Properties)

(unclaimed sequence; use of exendins and agonists thereof for modulation of triglyceride levels and treatment of dyslipidemia)

RE.CNT 7 THERE ARE 7 CITED REFERENCES AVAILABLE FOR THIS RECORD

RE

- (1) Amylin Pharmaceuticals Inc; WO 9830231 A 1998 HCAPLUS
- (2) Amylin Pharmaceuticals Inc; WO 0066629 A 2000 HCAPLUS
- (3) Andersson, K; WO 9962872 A 1999 HCAPLUS
- (4) Kolterman, O; DIABETOLOGIA, 36th Annual Meeting of the European Association for the Study of Diabetes 2000, V43(Supplement 1), PA189
- (5) Ligand Pharm Inc; WO 9805331 A 1998 HCAPLUS
- (6) Warner Lambert Co; WO 9930706 A 1999 HCAPLUS
- (7) Young, A; DIABETES 1999, V48, P1026 HCAPLUS

L30 ANSWER 3 OF '11 HCAPLUS COPYRIGHT 2003 ACS on STN

AN 2000:861704 HCAPLUS

DN 134:37033

ED Entered STN: 08 Dec 2000

TI Use of exendins and agonists thereof for the treatment of gestational diabetes mellitus

IN Hiles, Richard; Prickett, Kathryn S.

PA **Amylin Pharmaceuticals, Inc., USA**

SO PCT Int. Appl., 133 pp.

CODEN: PIXXD2

DT Patent

LA English

IC ICM C07K014-00

CC 1-10 (Pharmacology)

Section cross-reference(s): 34

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2000073331	A2	20001207	WO 2000-US14231	20000523 <--
	WO 2000073331	A3	20010628		
	W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
	RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG			
	US 6506724	B1	20030114	US 1999-323867	19990601 <--
	EP 1181043	A2	20020227	EP 2000-937710	20000523 <--
	R:	AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO			
	JP 2003501361	T2	20030114	JP 2001-500655	20000523 <--
PRAI	US 1999-323867	A	19990601	<--	
	WO 2000-US14231	W	20000523		

AB Methods for treating gestational diabetes which comprise administration of an effective amount of an exendin or an exendin agonist, alone or in conjunction with other compds. or compns. that lower blood glucose levels.

ST exendin agonist gestational diabetes mellitus treatment

IT Pregnancy

(gestational diabetes mellitus; use of exendins and agonists thereof for treatment of gestational diabetes mellitus in relation to combination with insulin or amylin agonist)

IT Diabetes mellitus
(gestational; use of exendins and agonists thereof for treatment of gestational diabetes mellitus in relation to combination with insulin or amylin agonist)

IT Antidiabetic agents
Drug interactions
(use of exendins and agonists thereof for treatment of gestational diabetes mellitus in relation to combination with insulin or amylin agonist)

IT 106602-62-4, Amylin
RL: BSU (Biological study, unclassified); BIOL (Biological study) (agonists; use of exendins and agonists thereof for treatment of gestational diabetes mellitus in relation to combination with insulin or amylin agonist)

IT 312949-28-3 312949-29-4 312949-30-7
RL: PRP (Properties)
(unclaimed protein sequence; use of exendins and agonists thereof for the treatment of gestational diabetes mellitus)

IT 210829-08-6P
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); SPN (Synthetic preparation); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(use of exendins and agonists thereof for treatment of gestational diabetes mellitus in relation to combination with insulin or amylin agonist)

IT **158345-16-5P 203743-29-7P 203743-31-1P**
203743-32-2P 203743-33-3P 203743-35-5P
203743-36-6P 203743-37-7P 203743-38-8P
203743-41-3P 203743-45-7P 203743-46-8P
203743-47-9P 203743-50-4P 210712-28-0P, 1-30-Exendin 4
(Heloderma suspectum) 210712-29-1P 210712-30-4P 210712-31-5P
210712-33-7P 210712-34-8P 210712-35-9P 210712-36-0P 210712-37-1P
210712-38-2P 210712-39-3P 210712-40-6P 210712-41-7P 210712-42-8P
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210712-86-0P 210712-87-1P 210712-88-2P 210712-89-3P 210712-90-6P
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210713-27-2P 210713-28-3P 210713-29-4P 210713-30-7P 210713-31-8P
210713-33-0P 210713-35-2P 210713-36-3P 210713-37-4P 210713-38-5P
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210828-38-9P 210828-61-8P 210828-91-4P 210828-92-5P 210828-93-6P
210829-01-9P 210829-03-1P 210829-04-2P 210829-11-1P 210829-12-2P
210829-35-9P 210829-39-3P 210829-43-9P 210829-44-0P 210829-45-1P
210829-56-4P 210829-57-5P 210829-59-7P 210829-60-0P 210829-61-1P
210830-02-7P 210830-13-0P 210830-14-1P 210830-15-2P
210830-22-1P 210830-29-8P **210830-35-6P 210830-59-4P**
238091-49-1P 238091-55-9P **284676-24-0P** 312925-05-6P
312925-06-7P 312925-07-8P 312925-08-9P 312925-09-0P 312925-10-3P
312932-20-0P 312932-28-8P 312932-49-3P 312932-83-5P
312933-83-8P 312949-21-6P 312949-26-1P
RL: BAC (Biological activity or effector, except adverse); BSU (Biological

study, unclassified); SPN (Synthetic preparation); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)

(use of exendins and agonists thereof for treatment of gestational diabetes mellitus in relation to combination with insulin or amylin agonist)

IT 9004-10-8, Insulin, biological studies 130357-25-4, Exendin 3 (Heloderma horridum) 141758-74-9, Exendin 4 (Heloderma suspectum) 203743-40-2 213190-65-9, Exendin

RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)

(use of exendins and agonists thereof for treatment of gestational diabetes mellitus in relation to combination with insulin or amylin agonist)

L30 ANSWER 4 OF 11 HCAPLUS COPYRIGHT 2003 ACS on STN

AN 2000:824301 HCAPLUS

DN 134:13338

ED Entered STN: 24 Nov 2000

TI Long lasting insulinotropic peptides

IN Bridon, Dominique P.; L'Archeveque, Benoit; Ezrin, Alan M.; Holmes, Darren L.; Leblanc, Anouk; St. Pierre, Serge

PA Conjuchem, Inc., Can.

SO PCT Int. Appl., 96 pp.

CODEN: PIXXD2

DT Patent

LA English

IC ICM C07K014-605

ICS C07K014-575; A61K038-26; A61P003-08

CC 1-10 (Pharmacology)

Section cross-reference(s): 2, 34

FAN.CNT 3

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2000069911	A1	20001123	WO 2000-US13563	20000517 <--
	W:	AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
	RW:	GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG			
	WO 2000070665	A2	20001123	WO 2000-IB763	20000517 <--
	WO 2000070665	A3	20010419		
	W:	AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW			
	RW:	GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG			
	EP 1171582	A2	20020116	EP 2000-929748	20000517 <--
	R:	AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO			
	EP 1180121	A1	20020220	EP 2000-930796	20000517 <--
	EP 1180121	B1	20031022		
	R:	AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO			
	BR 2000010750	A	20020226	BR 2000-10750	20000517 <--

AU 754770	B2	20021121	AU 2000-48555	20000517 <--
EP 1264840	A1	20021211	EP 2002-14617	20000517 <--
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL				
JP 2003500341	T2	20030107	JP 2000-619018	20000517 <--
JP 2003527312	T2	20030916	JP 2000-618327	20000517 <--
US 6329336	B1	20011211	US 2000-623618	20000905 <--
US 6514500	B1	20030204	US 2000-657332	20000907 <--
US 2002049153	A1	20020425	US 2001-876388	20010606 <--
US 6593295	B2	20030715		
ZA 2001006676	A	20020719	ZA 2001-6676	20010814 <--
ZA 2001009110	A	20020613	ZA 2001-9110	20011105 <--
NO 2001005584	A	20020103	NO 2001-5584	20011115 <--
US 2003108567	A1	20030612	US 2002-287892	20021104 <--
US 2003108568	A1	20030612	US 2002-288340	20021104 <--
PRAI US 1999-134406P	P	19990517	<--	
US 1999-159783P	P	19991015	<--	
US 1999-153406P	P	19990910	<--	
EP 2000-932570	A3	20000517		
WO 2000-IB763	W	20000517		
WO 2000-US13563	W	20000517		
US 2000-623618	A3	20000905		
US 2000-657332	A3	20000907		
AB	Modified insulinotropic peptides are disclosed. The modified insulinotropic peptides are capable of forming a peptidase stabilized insulinotropic peptide. The modified insulinotropic peptides are capable of forming covalent bonds with one or more blood components to form a conjugate. The conjugates may be formed in vivo or ex vivo. The modified peptides are administered to treat humans with diabetes and other related diseases.			
ST	insulinotropic peptide prepn blood covalent bond; antidiabetic insulinotropic peptide			
IT	Sulfhydryl group (blood protein; long lasting insulinotropic peptides with antidiabetic activity)			
IT	Blood (components, covalent bonds; long lasting insulinotropic peptides with antidiabetic activity)			
IT	Antidiabetic agents (long lasting insulinotropic peptides with antidiabetic activity)			
IT	Peptides, biological studies RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses) (long lasting insulinotropic peptides with antidiabetic activity)			
IT	309729-73-5 RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses) (lasting insulinotropic pepwith antidiabetic activity)			
IT	87805-34-3, Glucagon-like peptide I (human) 106612-94-6 165338-06-7 203743-40-2 306277-48-5 308239-12-5 308240-40-6 308243-89-2 308245-55-8 308348-98-3 308348-99-4 308349-00-0 308349-01-1 308349-02-2 308349-03-3 308349-04-4 308349-05-5 308349-06-6 308349-07-7 308349-08-8 308349-09-9 308805-99-4 308806-00-0 308806-01-1 308806-02-2 308815-99-8 309729-06-4 309729-11-1 309729-42-8 309729-80-4 RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses) (long lasting insulinotropic peptides with antidiabetic activity)			
IT	9004-10-8, Insulin, biological studies RL: BSU (Biological study, unclassified); BIOL (Biological study)			

(long lasting insulinitropic peptides with antidiabetic activity)

IT 130357-25-4P, Exendin 3 (Heloderma horridum) 307314-60-9P 307315-09-9P
 307493-98-7P 308239-65-8P 308240-57-5P 308244-15-7P
308244-92-0P 308249-19-6P 308348-96-1P 308348-97-2P
 308805-98-3P **309728-25-4P** 309729-07-5P 309729-12-2P
 309729-72-4P **309729-78-0P 309729-82-6P**

RL: SPN (Synthetic preparation); PREP (Preparation)

(long lasting insulinitropic peptides with antidiabetic activity)

RE.CNT 6 THERE ARE 6 CITED REFERENCES AVAILABLE FOR THIS RECORD

RE

- (1) Conjuchem Inc; WO 9924074 A 1999 HCAPLUS
- (2) Conjuchem Inc; WO 9924075 A 1999 HCAPLUS
- (3) Conjuchem Inc; WO 9948536 A 1999 HCAPLUS
- (4) Hancock, W; US 5614487 A 1997 HCAPLUS
- (5) Pouletty, P; EP 0602290 A 1994 HCAPLUS
- (6) Redcell Inc; WO 9510302 A 1995 HCAPLUS

L30 ANSWER 5 OF 11 HCAPLUS COPYRIGHT 2003 ACS on STN

AN 2000:824291 HCAPLUS

DN 134:21425

ED Entered STN: 24 Nov 2000

TI Protection of endogenous therapeutic peptides from peptidase activity
 through conjugation to blood components

IN Bridon, Dominique P.; Ezrin, Alan M.; Milner, Peter G.; Holmes, Darren L.;
 Thibaudeau, Karen

PA Conjuchem, Inc., Can.

SO PCT Int. Appl., 733 pp.

CODEN: PIXXD2

DT Patent

LA English

IC ICM C07K014-00

CC 63-3 (Pharmaceuticals)

Section cross-reference(s): 34

FAN.CNT 3

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2000069900	A2	20001123	WO 2000-US13576	20000517 <--
	WO 2000069900	A3	20010215		
	WO 2000069900	C2	20020704		
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	RW:		GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG		
	WO 2000070665	A2	20001123	WO 2000-IB763	20000517 <--
	WO 2000070665	A3	20010419		
	W:		AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW		
	RW:		GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG		
EP 1105409	A2	20010613	EP 2000-936023	20000517 <--	
	R:		AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO		
EP 1171582	A2	20020116	EP 2000-929748	20000517 <--	

R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO

EP 1264840 A1 20021211 EP 2002-14617 20000517 <--
 R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL

JP 2003500341 T2 20030107 JP 2000-619018 20000517 <--
 JP 2003508350 T2 20030304 JP 2000-618316 20000517 <--
 AU 765753 B2 20030925 AU 2000-51393 20000517 <--
 US 6514500 B1 20030204 US 2000-657332 20000907 <--
 ZA 2001006676 A 20020719 ZA 2001-6676 20010814 <--
 ZA 2001009110 A 20020613 ZA 2001-9110 20011105 <--
 US 2003108567 A1 20030612 US 2002-287892 20021104 <--
 US 2003108568 A1 20030612 US 2002-288340 20021104 <--

PRAI US 1999-134406P P 19990517 <--
 US 1999-153406P P 19990910 <--
 US 1999-159783P P 19991015 <--
 EP 2000-932570 A3 20000517
 WO 2000-IB763 W 20000517
 WO 2000-US13576 W 20000517
 US 2000-657332 A3 20000907

AB A method for protecting a peptide from peptidase activity in vivo, the peptide being composed of between 2 and 50 amino acids and having a C-terminus and an N-terminus and a C-terminus amino acid and an N-terminus amino acid is described. In the first step of the method, the peptide is modified by attaching a reactive group to the C-terminus amino acid, to the N-terminus amino acid, or to an amino acid located between the N-terminus and the C-terminus, such that the modified peptide is capable of forming a covalent bond in vivo with a reactive functionality on a blood component. The solid phase peptide synthesis of a number of derivs. with 3-maleimidopropionic acid (3-MPA) is described. In the next step, a covalent bond is formed between the reactive group and a reactive functionality on a blood component to form a peptide-blood component conjugate, thereby protecting said peptide from peptidase activity. The final step of the method involves the analyzing of the stability of the peptide-blood component conjugate to assess the protection of the peptide from peptidase activity. Thus, the percentage of a K5 kringle peptide (Pro-Arg-Lys-Leu-Tyr-Asp-Lys-NH₂) conjugated to human serum albumin via MPA remained relatively constant through a 24-h plasma assay in contrast to unmodified K5 which decreased to 9% of the original amount of K5 in only 4 h in plasma.

ST therapeutic peptide conjugation blood albumin stability; peptidase stability therapeutic peptide conjugate blood; maleimido conjugation therapeutic peptide peptidase stability

IT Proteins, specific or class
 RL: BPR (Biological process); BSU (Biological study, unclassified); SPN (Synthetic preparation); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); PROC (Process); USES (Uses)
 (CART (cocaine and amphetamine-regulated transcript); protection of endogenous therapeutic peptides from peptidase activity through conjugation to blood components)

IT Proteins, specific or class
 RL: BPR (Biological process); BSU (Biological study, unclassified); SPN (Synthetic preparation); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); PROC (Process); USES (Uses)
 (apoptosis-regulating; protection of endogenous therapeutic peptides from peptidase activity through conjugation to blood components)

IT Proteins, general, biological studies
 RL: SPN (Synthetic preparation); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
 (blood, conjugates; protection of endogenous therapeutic peptides from peptidase activity through conjugation to blood components)

IT Peptides, biological studies
 RL: BPR (Biological process); BSU (Biological study, unclassified); SPN

- (Synthetic preparation); THU (Therapeutic use); BIOL (Biological study);
 PREP (Preparation); PROC (Process); USES (Uses)
 (conjugates, therapeutic; protection of endogenous therapeutic peptides
 from peptidase activity through conjugation to blood components)
- IT Fibrinogen degradation products
 RL: BPR (Biological process); BSU (Biological study, unclassified); SPN
 (Synthetic preparation); THU (Therapeutic use); BIOL (Biological study);
 PREP (Preparation); PROC (Process); USES (Uses)
 (fibrinopeptides; protection of endogenous therapeutic peptides from
 peptidase activity through conjugation to blood components)
- IT Fibronectins
 Laminins
 RL: BPR (Biological process); BSU (Biological study, unclassified); SPN
 (Synthetic preparation); THU (Therapeutic use); BIOL (Biological study);
 PREP (Preparation); PROC (Process); USES (Uses)
 (fragments; protection of endogenous therapeutic peptides from
 peptidase activity through conjugation to blood components)
- IT Complement
 RL: BPR (Biological process); BSU (Biological study, unclassified); SPN
 (Synthetic preparation); THU (Therapeutic use); BIOL (Biological study);
 PREP (Preparation); PROC (Process); USES (Uses)
 (inhibitors; protection of endogenous therapeutic peptides from
 peptidase activity through conjugation to blood components)
- IT Functional groups
 (maleimido or succinimidyl; protection of endogenous therapeutic
 peptides from peptidase activity through conjugation to blood
 components)
- IT Solid phase synthesis
 (peptide; protection of endogenous therapeutic peptides from peptidase
 activity through conjugation to blood components)
- IT Antimicrobial agents
 Antioxidants
 Signal transduction, biological
 (peptides; protection of endogenous therapeutic peptides from peptidase
 activity through conjugation to blood components)
- IT Cell adhesion molecules
 Chemotactic factors
 G proteins (guanine nucleotide-binding proteins)
 Gastrointestinal hormones
 Hypothalamic hormones
 Interleukin receptors
 Interleukins
 Osteocalcins
 Pancreatic hormones
 Pituitary hormones
 Tachykinins
 Thyroid hormones
 Toxins
 RL: BPR (Biological process); BSU (Biological study, unclassified); SPN
 (Synthetic preparation); THU (Therapeutic use); BIOL (Biological study);
 PREP (Preparation); PROC (Process); USES (Uses)
 (protection of endogenous therapeutic peptides from peptidase activity
 through conjugation to blood components)
- IT Albumins, biological studies
 RL: SPN (Synthetic preparation); THU (Therapeutic use); BIOL (Biological
 study); PREP (Preparation); USES (Uses)
 (serum, conjugates; protection of endogenous therapeutic peptides from
 peptidase activity through conjugation to blood components)
- IT Amyloid
 RL: BPR (Biological process); BSU (Biological study, unclassified); SPN
 (Synthetic preparation); THU (Therapeutic use); BIOL (Biological study);
 PREP (Preparation); PROC (Process); USES (Uses)
 (β -, fragments; protection of endogenous therapeutic peptides from

- peptidase activity through conjugation to blood components)
- IT 124219-00-7
RL: PRP (Properties)
(Unclaimed; protection of endogenous therapeutic peptides from
peptidase activity through conjugation to blood components)
- IT 169494-85-3P, Leptin
RL: BPR (Biological process); BSU (Biological study, unclassified); SPN
(Synthetic preparation); THU (Therapeutic use); BIOL (Biological study);
PREP (Preparation); PROC (Process); USES (Uses)
(fragments; protection of endogenous therapeutic peptides from
peptidase activity through conjugation to blood components)
- IT 9002-04-4P, Thrombin
RL: BPR (Biological process); BSU (Biological study, unclassified); SPN
(Synthetic preparation); THU (Therapeutic use); BIOL (Biological study);
PREP (Preparation); PROC (Process); USES (Uses)
(inhibitors; protection of endogenous therapeutic peptides from
peptidase activity through conjugation to blood components)
- IT 9031-96-3, Peptidase
RL: BAC (Biological activity or effector, except adverse); BSU (Biological
study, unclassified); BIOL (Biological study)
(protection of endogenous therapeutic peptides from peptidase activity
through conjugation to blood components)
- IT 50-56-6P, Oxytocin, biological studies 1393-25-5P, Secretin
1407-47-2P, Angiotensin 9002-60-2P, ACTH, biological studies
9002-64-6P, Parathyroid hormone 9002-72-6P, Growth hormone 9002-76-0P,
Gastrin 9002-79-3P, MSH 9004-10-8P, Insulin, biological studies
9007-12-9P, Calcitonin 9007-92-5P, Glucagon, biological studies
9011-97-6P, Cholecystokinin 9015-71-8P, Corticotropin-releasing factor
9034-39-3P, Growth hormone-releasing factor 9034-40-6P, Luteinizing
hormone-releasing factor 9035-81-8P, Trypsin inhibitor 9088-07-7P,
Natriuretic peptide 11000-17-2P, Vasopressin 24305-27-9P,
Thyrotropin-releasing hormone 31362-50-2P, Bombesin 37221-79-7P,
Vasoactive intestinal polypeptide 38916-34-6P, Somatostatin
39362-14-6P, Prolactin-releasing factor 52906-92-0P, Motilin
57285-09-3P, Inhibin 58391-28-9P, Leukokinins 59763-91-6P, Pancreatic
polypeptide 64190-70-1P, FMRFamide 73019-95-1P, Egg-laying hormone
80043-53-4P, Gastrin-releasing peptide 81858-94-8P, Peptide YY (swine)
82785-45-3P, Neuropeptide Y 83652-28-2P, Calcitonin gene related peptide
85637-73-6P, Atrial natriuretic peptide 103370-86-1P, Parathormone-like
peptide 106602-62-4P, Amylin 107666-54-6P, Gonadotropin-releasing
hormone-associated peptide 114471-18-0P, Brain natriuretic peptide
116110-78-2P, Insulin-like peptide 117148-67-1P, Pancreastatin
119418-04-1P, Galanin 127830-04-0P, C-Type natriuretic peptide
137061-48-4P, Pituitary adenylate cyclase-activating polypeptide
144940-98-7P, Guanylin 164252-35-1P, Uroguanylin 193829-96-8P,
Cortistatin 245359-74-4P, Orexin
RL: BPR (Biological process); BSU (Biological study, unclassified); SPN
(Synthetic preparation); THU (Therapeutic use); BIOL (Biological study);
PREP (Preparation); PROC (Process); USES (Uses)
(protection of endogenous therapeutic peptides from peptidase activity
through conjugation to blood components)
- IT 6066-82-6, N-Hydroxysuccinimide 7423-55-4, 3-Maleimidopropionic acid
82436-78-0, N-Hydroxysulfosuccinimide
RL: RCT (Reactant); RACT (Reactant or reagent)
(protection of endogenous therapeutic peptides from peptidase activity
through conjugation to blood components)
- IT 224785-55-1P 224785-57-3P 224785-59-5P 224785-62-0P 307314-48-3P
307314-50-7P 307314-52-9P 307314-54-1P 307314-56-3P 307314-57-4P
307314-59-6P 307314-60-9P 307314-61-0P 307314-63-2P 307314-65-4P
307314-67-6P 307314-69-8P 307314-71-2P 307314-73-4P 307314-75-6P
307314-77-8P 307314-78-9P 307314-79-0P 307314-80-3P 307314-82-5P
307314-84-7P 307314-86-9P 307314-88-1P 307314-90-5P 307314-92-7P
307314-94-9P 307314-96-1P 307314-98-3P 307315-00-0P 307315-02-2P

307315-04-4P 307315-06-6P 307315-08-8P 307315-09-9P 307315-10-2P
 307315-11-3P 307315-13-5P 307315-14-6P 307315-15-7P 307315-16-8P
 307315-17-9P 307315-18-0P 307315-19-1P 307315-20-4P 307493-39-6P
 307493-98-7P 307494-76-4P 307494-77-5P 307494-92-4P 307494-93-5P
 308239-65-8P 308240-25-7P 308240-57-5P 308242-06-0P 308244-15-7P
 308244-75-9P 308245-14-9P 308245-46-7P

308249-19-6P 308249-28-7P 308277-45-4P 308277-79-4P

RL: RCT (Reactant); SPN (Synthetic preparation); THU (Therapeutic use);
 BIOL (Biological study); PREP (Preparation); RACT (Reactant or reagent);
 USES (Uses)

(protection of endogenous therapeutic peptides from peptidase activity
 through conjugation to blood components)

IT 307315-20-4DP, conjugate with human serum albumin

RL: SPN (Synthetic preparation); THU (Therapeutic use); BIOL (Biological
 study); PREP (Preparation); USES (Uses)

(protection of endogenous therapeutic peptides from peptidase activity
 through conjugation to blood components)

IT 9015-94-5P, Renin, biological studies

RL: BPR (Biological process); BSU (Biological study, unclassified); SPN
 (Synthetic preparation); THU (Therapeutic use); BIOL (Biological study);
 PREP (Preparation); PROC (Process); USES (Uses)

(substrates and inhibitors; protection of endogenous therapeutic
 peptides from peptidase activity through conjugation to blood
 components)

IT 11063-17-5, Gastric inhibitory polypeptide (swine major) 12279-41-3,
 α 1-39-Corticotropin (human) 51257-86-4 52232-67-4 68563-24-6,
 Corticotropin-inhibiting peptide (human) 75718-92-2, Peptide F (cattle
 adrenal medulla) 77465-10-2, α 1-39-Corticotropin (rat)
 82707-63-9 83328-95-4, Dynorphin-32 (swine) 84069-10-3,
 1-40-Somatoliberin (human pancreatic islet) 84136-38-9,
 1-37-Somatoliberin (human pancreatic islet) 85568-24-7,
 1-44-Parathormone (human) 86472-71-1, Somatoliberin (rat hypothalamus)
 86546-19-2 87713-86-8, Peptide B (cattle adrenal medulla) 87805-34-3,
 Glucagon-like peptide I (human) 88402-03-3, Defensin NP 3A (rabbit
 reduced) 89492-47-7 89747-89-7, Transforming growth factor α
 (rat reduced) 90599-39-6 90880-43-6 92879-83-9, α -Inhibin-31
 (human seminal plasma) 96351-01-8 96827-07-5 98226-75-6 98614-76-7
 99120-49-7, Glucagon-like peptide II (human) 99658-03-4 99658-10-3
 100040-31-1, Gastric inhibitory polypeptide (human) 100915-92-2
 101178-74-9 107761-42-2, Glycopeptide (human clone 9-110 amyloid A4
 peptide moiety) 110616-04-1 111274-30-7, Pancreatic polypeptide (Canis
 familiaris) 111366-38-2 112199-06-1 112540-82-6 112602-83-2,
 Somatoliberin (carp) 112938-42-8 116977-48-1, Defensin NP 4 (human
 reduced) 118277-01-3 118337-11-4, Echistatin α 1 (reduced)
 119977-20-7 120298-73-9 121181-17-7, Glucagon-like peptide 1 (Octodon
 degus) 122931-92-4 123337-90-6, Brain natriuretic peptide-45 (rat
 reduced) 123757-43-7 124147-28-0, Lymphokine CINC (rat subunit
 reduced) 124541-50-0 124834-82-8 124834-83-9 125199-49-7,
 Somatoliberin (mouse) 126466-47-5 126466-48-6 127609-05-6
 128906-76-3, Decorsin (reduced) 129405-61-4 131438-74-9 131438-79-4
 134090-87-2 134500-80-4 134710-25-1, Calciseptin (Dendroaspis
 polylepis polylepis reduced) 135842-15-8 136751-54-7, C-Type
 natriuretic peptide (human clone λ hCNP 53-amino acid isoform
 reduced) 137467-72-2, C-Type natriuretic peptide (swine clone
 λ CNP6 53-amino acid isoform reduced) 138634-59-0 139872-85-8
 141983-93-9 142192-88-9 142297-36-7 144409-98-3 144409-99-4
 144855-49-2 146103-03-9 148846-98-4, Brain natriuretic peptide-45
 (mouse reduced) 150679-91-7 150680-28-7, Adrenomedullin (human clone
 PHAM-3) 150871-76-4 151247-82-4, Margatoxin (reduced) 154101-11-8
 155420-59-0 155924-66-6 157938-23-3 161246-49-7 161246-56-6
 161246-57-7 161246-58-8 161246-60-2 161246-61-3 161246-62-4
 161246-63-5 161246-67-9 161246-68-0 161246-69-1 161246-72-6
 161246-74-8 161246-75-9 161246-87-3 161246-92-0 161246-93-1

161246-94-2	161247-04-7	161247-06-9	161247-07-0	161247-08-1
161247-09-2	161247-11-6	161247-12-7	161247-16-1	161247-21-8
161247-23-0	161247-24-1	161247-34-3	161247-35-4	161247-37-6
161247-48-9	161247-49-0	161247-50-3	161247-56-9	161247-58-1
161247-61-6	161278-54-2	161818-07-1, Endothelin 3 (rat reduced)		
164714-89-0, ω -Agatoxin TK 2 (reduced)	165168-50-3, Toxin ShK			
(Stoichactis helianthus potassium-channel reduced)	166090-74-0			
166798-69-2	171543-83-2, Urocortin (Rattus norvegicus)	173010-28-1,		
Buforin I	174394-41-3	175524-68-2, Glucagon-like peptide 1 (Amphiuma tridactylum)		
	175779-77-8,	Glucagon-like peptide 2 (Amphiuma tridactylum)		
179733-43-8	179733-44-9	183598-56-3	183681-18-7	184007-69-0
186322-91-8	186673-12-1	186673-13-2	186673-14-3	186673-15-4
186673-16-5	186673-17-6	186673-18-7	186673-19-8	186673-20-1
186673-21-2	186811-41-6	187111-84-8	187111-86-0	187111-91-7
187547-59-7	188762-99-4	192588-09-3	192588-12-8	195262-56-7
203265-23-0	203743-40-2	206010-80-2	208540-81-2	211496-36-5
213779-10-3	213779-21-6	221377-92-0	227015-70-5	235787-61-8
256345-50-3	256345-87-6	256345-89-8	256345-94-5	256345-97-8
256345-99-0	256346-01-7	256346-36-8	256346-45-9	256346-54-0
256346-89-1	256346-91-5	260363-52-8	302905-40-4	303052-45-1
306277-48-5	308388-50-3	309255-20-7	309255-24-1	309255-30-9
309255-32-1	309255-44-5	309255-50-3	309255-60-5	309255-62-7
309255-64-9	309255-68-3	309255-69-4	309255-71-8	309255-72-9
309255-73-0	309255-74-1	309255-75-2	309255-76-3	309255-77-4
309255-78-5	309255-79-6	309255-80-9	309255-81-0	309255-91-2
309256-41-5	309256-67-5	309257-14-5	309257-15-6	
309257-17-8	309257-18-9	309257-19-0	309257-20-3	
309257-21-4	309257-22-5	309257-23-6	309257-26-9	309257-27-0
309257-32-7	309257-33-8	309257-34-9	309257-46-3	309260-49-9
309260-50-2	309260-58-0	309260-63-7	309260-66-0	309260-67-1
309260-68-2	309260-69-3	309260-72-8	309260-73-9	309260-74-0
309260-75-1	309260-76-2	309260-77-3		

RL: PRP (Properties)

(unclaimed protein sequence; protection of endogenous therapeutic peptides from peptidase activity through conjugation to blood components)

IT	309260-78-4	309260-79-5	309260-80-8	309262-13-3	309262-14-4
	309262-15-5	309262-16-6	309262-17-7	309262-19-9	309262-20-2
	309262-21-3	309262-22-4	309262-23-5	309262-24-6	309262-25-7
	309262-26-8	309262-27-9	309262-28-0	309262-29-1	309262-30-4
	309262-40-6	309262-41-7	309262-42-8	309262-43-9	309262-44-0
	309262-45-1	309262-47-3	309262-50-8	309262-51-9	309262-55-3
	309262-56-4	309262-57-5	309262-59-7	309262-60-0	309262-61-1
	309290-71-9	309291-04-1	309294-09-5		

RL: PRP (Properties)

(unclaimed protein sequence; protection of endogenous therapeutic peptides from peptidase activity through conjugation to blood components)

IT	53-73-6	58-49-1	484-42-4	484-43-5	4037-01-8	4086-29-7
	4474-91-3	5576-42-1, α 1-16-Corticotropin	7266-47-9,			
	α 1-17-Corticotropin	9063-57-4	9072-41-7, Motilin (swine)			
	10587-93-6	13602-53-4	16322-68-2	16376-83-3	16941-32-5, Glucagon	
	(swine)	16960-16-0, α 1-24-Corticotropin	17908-57-5,			
	β -Melanotropin (human)	19941-13-0, β -Melanotropin (swine)				
	20845-02-7	22006-64-0, α 1-13-Corticotropin	23025-68-5			
	25422-31-5, Fibrinopeptide A (human)	26251-06-9	32204-93-6			
	32222-04-1	33017-11-7, Proinsulin C-peptide (human)	33512-65-1,			
	α 6-24-Corticotropin	34233-50-6	35144-91-3	37548-29-1,		
	β -Cell-tropin (human)	38023-98-2	40958-31-4, Somatostatin (sheep			
	reduced)	49759-44-6	51006-12-3	51833-78-4	52498-25-6, Angiotensin	
	III inhibitor (human)	52530-60-6	52580-29-7	53917-42-3	55207-83-5	
	55714-12-0	56317-01-2	56767-30-7	56795-64-3	57327-90-9	
	57468-16-3	57468-17-4, 1-9-Substance P	57866-92-9	57899-85-1		

58108-03-5 58569-55-4, 1-5-Adrenorphin (human) 58822-25-6,
 1-5- β -Neoendorphin (human) 59004-96-5, α -Endorphin (sheep)
 59481-79-7, 1-9- α -Endorphin (sheep) 59530-69-7 59587-18-7
 59887-17-1, β -Endorphin (sheep) 60030-26-4 60030-27-5
 60149-45-3, β -Endorphin (swine) 60254-81-1 60254-82-2
 60254-83-3 60284-47-1 60556-70-9 60703-95-9 60893-02-9,
 γ -Endorphin (human) 61214-51-5, β -Endorphin (human)
 61756-22-7 61756-28-3 62568-57-4, Delta sleep-inducing peptide
 (rabbit) 63058-21-9 63373-83-1 63642-75-1 64421-69-8 64790-15-4
 65189-70-0 65418-88-4 65505-61-5 66954-40-3, 80-Endorphin
 (cattle) 67083-30-1 67224-41-3 67746-47-8 67810-56-4 68060-49-1,
 1-7-Substance P 68102-99-8, 1-26- β -Endorphin (sheep) 68232-52-0,
 1-6-Substance P 68374-46-9 68375-78-0 69361-26-8 69558-55-0
 70534-26-8, 2-9-Thymulin (swine peptide moiety) 70920-39-7 71494-20-7
 71823-87-5 71823-88-6 71977-09-8 72007-47-7 72122-62-4 72122-63-5
 72189-84-5 72601-97-9 72645-79-5, γ -Melanotropin (human)
 72957-38-1, 1-13-Dynorphin A (swine) 73024-95-0 73726-64-4,
 1-10-Substance P 73984-05-1 74012-06-9 74171-19-0 74216-35-6
 74221-77-5 75106-71-7 75106-72-8 75148-76-4 75306-06-8,
 Somatostatin-28 (sheep reduced) 75513-71-2 75567-52-1 75645-19-1
 75909-25-0 76310-14-0, 1-6-Adrenorphin (human) 76496-10-1
 76622-26-9, 1-22-Peptide E (cattle adrenal medulla) 76622-84-9,
 1-27- β -Endorphin (human) 76901-59-2, Sperm-activating peptide H 2
 (Hemicentrotus pulcherrimus egg jelly coat) 77654-52-5 77727-17-4
 77739-20-9, α -Neoendorphin (swine) 77739-21-0, β -Neoendorphin
 (human) 77761-27-4, 6-31- β -Endorphin (human) 77875-68-4
 78151-11-8 78355-50-7, Peptide E (cattle adrenal medulla) 79243-10-0
 79358-92-2 79495-86-6, β -Endorphin (horse) 79515-35-8
 79985-35-6, 1-12-Dynorphin A (swine) 79994-24-4, 1-10-Dynorphin A
 (swine) 80237-40-7 80244-69-5, Calcitonin C-peptide (rat)
 80448-90-4, Dynorphin A (swine) 80501-44-6 80755-86-8 80790-40-5
 80943-05-1 81286-16-0 81306-64-1 81478-67-3 81493-98-3
 81643-78-9, Urotensin II (Gillichthys mirabilis reduced) 82048-97-3
 82177-09-1 83286-22-0 83335-41-5, Dynorphin B (swine) 83404-42-6
 83404-43-7 83471-50-5 83608-80-4, 2-17-Dynorphin A (swine)
 84376-30-7, Leumorphin (swine) 84745-13-1 85344-34-9 85490-53-5,
 Motilin (Canis familiaris) 85916-47-8, Katalcalcin (human) 86555-35-3
 86879-15-4 87079-95-6, 6-17-Dynorphin A (swine) 87549-52-8,
 α -Bag cell peptide (Aplysia californica) 87549-53-9 87549-54-0
 88846-98-4, Leumorphin (human) 88866-92-6 89106-96-7, Atrial
 natriuretic peptide-21 (rat reduced) 89202-80-2, 3-13-Dynorphin A
 (swine) 89458-24-2 90686-51-4 90830-28-7, 1-29-Somatoliberin (human
 pancreatic islet) 91037-65-9 91037-75-1 91575-25-6 91575-26-7
 91853-94-0 91917-63-4, Atrial natriuretic peptide-28 (human reduced)
 91999-74-5 92169-45-4, Neuromedin N (swine spinal cord) 92952-95-9
 93511-94-5 93590-01-3, Atrial natriuretic peptide-26 (rat reduced)
 93674-95-4 93674-97-6 93674-99-8 93675-01-5 94773-24-7
 95211-04-4 95480-66-3, Atrial natriuretic peptide-25 (rat reduced)
 95480-67-4, Atrial natriuretic peptide-24 (rat reduced) 95480-70-9,
 Atrial natriuretic peptide-23 (rat reduced) 95596-38-6 96031-58-2
 96249-43-3 96426-21-0 96573-46-5 96573-86-3, Atrial natriuretic
 peptide-24 (human reduced) 96573-88-5, Atrial natriuretic peptide-23
 (human reduced) 96573-89-6, Atrial natriuretic peptide-28 (rat reduced)
 96611-51-7, 1-24-Atrial natriuretic peptide-25 (rat reduced) 96663-13-7,
 9-17-Dynorphin A (swine) 97461-82-0 97461-84-2 98897-21-3
 99027-06-2 99273-04-8 99278-03-2 99287-07-7, Defensin NP 2 (human
 reduced) 99287-08-8, Defensin NP 1 (human reduced) 99291-20-0
 99694-34-5 99896-86-3 99896-88-5 10011-07-7 100691-58-5, Atrial
 natriuretic peptide-26 (human reduced) 100808-57-9 100815-33-6
 101038-77-1 101038-78-2 101038-79-3 101038-80-6 101038-81-7
 101214-33-9 101455-37-2 101641-70-7 102029-74-3 102910-14-5,
 8-17-Dynorphin A (swine) 102989-34-4 103131-69-7, Kinetensin (human)
 103213-49-6 103217-01-2 103217-13-6 103226-11-5 103244-41-3

RL: PRP (Properties)

(unclaimed sequence; protection of endogenous therapeutic peptides from
peptidase activity through conjugation to blood components)

IT 103424-74-4 103974-46-5 104180-23-6 104413-56-1 104504-34-9
104914-40-1 105284-56-8, 1-18-Peptide E (cattle adrenal medulla)
105416-63-5, Atrial natriuretic peptide-25 (human reduced) 105464-22-0
105553-21-7 105802-82-2 105802-84-4 106021-67-4 106021-96-9
106061-19-2 106362-32-7 106686-61-7 106897-47-6 106897-48-7
107015-83-8 107489-37-2, Thymic humoral factor γ 2 (cattle)
107902-86-3 107978-83-6 108334-68-5 108433-95-0, Magainin II
108433-99-4, Magainin I 108548-50-1 108608-63-5 108682-58-2
109024-47-7 109024-48-8 109292-46-8 109708-36-3 109708-37-4
109770-29-8, 1-28-Glycopeptide (human clone 9-110 amyloid A4 peptide
moiety) 109796-64-7 110121-11-4 110200-37-8 110590-64-2
110697-44-4 110713-84-3 110765-06-5, 7-17-Dynorphin A (swine)
112160-82-4 112160-83-5 112173-49-6 113194-00-6 113480-19-6
113846-80-3 113851-71-1 113944-46-0 114400-89-4, Brain natriuretic
peptide-26 (swine reduced) 114495-85-1 114640-06-1, Endothelin 1
(swine reduced) 114681-65-1 114991-28-5 115044-69-4 115136-18-0
115722-31-1 115918-58-6 116303-65-2, Sarafotoxin S 6b (reduced)
116331-69-2 116495-45-5, Sarafotoxin S 6c (reduced) 116729-33-0
116872-17-4 116920-16-2 117038-68-3 117137-85-6 117620-76-5
117788-28-0, Sperm-activating peptide B (Glyptocidaris crenularis egg
jelly coat reduced) 118068-30-7 118473-55-5, Atrial natriuretic
peptide-29 (chicken reduced) 118691-41-1, Atrial natriuretic peptide-24
(Rana catesbeiana reduced) 118691-42-2, Atrial natriuretic peptide-21
(Rana catesbeiana reduced) 118934-21-7 119222-85-4 119320-26-2,
Brain natriuretic peptide-32 (swine reduced) 119777-39-8 119798-33-3
119965-38-7, Sarafotoxin S 6a (reduced) 120372-50-1 120550-85-8
120928-03-2 120928-04-3, Endothelin 2 (mouse reduced) 121204-87-3
121284-21-7 121369-79-7 121377-67-1 121379-63-3 121798-56-9
121873-03-8, Endothelin 2 (Canis familiaris reduced) 121880-96-4
121892-55-5, Endothelin 3 (human clone λ ghET-3 reduced)
122018-91-1 122680-32-4, Proinsulin C-peptide (Anguilla anguilla)
123025-94-5 123148-51-6 123168-46-7 123402-49-3 123402-50-6
123475-27-4 123924-45-8, 14-45-Brain natriuretic peptide-45 (rat
reduced) 124052-07-9 124210-91-9 124361-60-0, Sarafotoxin S 6d
(reduced) 124373-02-0 124932-61-2 125118-77-6, 1-16-Galanin (rat)
125408-80-2, 1-24-Neuropeptide K (swine) 125455-58-5 125651-07-2
125720-21-0 126035-36-7 126050-26-8, 1-9-Dynorphin B (swine)
126144-46-5 126646-77-3 126768-94-3 127007-82-3 127119-75-9
127574-55-4, C-Type natriuretic peptide-22 (swine reduced) 128439-39-4
128578-18-7 128746-58-7, 3-24-Atrial natriuretic peptide-24 (human
reduced) 128858-09-3 129015-19-6 129047-99-0 129437-45-2
129449-07-6 129761-58-6 129822-19-1 130444-07-4 130571-15-2
130571-28-7 130596-11-1 130734-57-5 130839-37-1 131023-24-0
131204-46-1 131602-53-4 132633-98-8 132769-35-8 132796-64-6
132996-61-3, Osteogenic growth peptide (human) 133474-20-1 133563-20-9
133605-53-5 133605-55-7 133633-11-1 133920-04-4 134000-89-8
134027-58-0 134282-68-1 134314-61-7 134374-28-0 134562-79-1
134580-64-6 134649-74-4 134824-87-6 134861-50-0 134875-67-5,
1-30-Gastric inhibitory polypeptide (swine major) 135131-17-8
135861-49-3 135861-77-7 136005-51-1, 1-19-Galanin (human)
136024-41-4, Galanin (human) 136033-70-0, Dermaseptin I (Phyllomedusa
sauvagei) 136466-51-8 136831-50-0 137110-97-5 137181-56-7
137187-39-4 137350-87-9 137350-89-1 137622-06-1 137833-31-9,
Myelopeptide 2 137859-81-5 138039-25-5 138506-90-8 138831-86-4
138949-73-2 139031-15-5 139446-70-1 139579-35-4 140653-38-9,
Guanylin (rat reduced) 142385-09-9 142547-17-9, Bactenecin (reduced)
142828-10-2 142878-29-3 142998-27-4 143257-74-3 143257-75-4
143784-00-3 143896-15-5 143909-59-5 144092-28-4 144110-41-8
144189-71-9 144313-54-2, Valorphin (cattle) 144450-06-6 144704-36-9
144860-95-7 145143-20-0 145194-22-5 145224-96-0 145224-99-3

145319-90-0, Guanylin (human reduced)	145569-99-9	145852-04-6
147138-56-5	147262-52-0	147740-73-6
148067-21-4	148914-01-6	148914-08-3
149839-93-0	149839-94-1	150034-08-5
150944-04-0	150944-05-1	151151-30-3
152051-21-3	152051-62-2	152129-87-8
2-12-Dynorphin A (swine)	153538-69-3,	3-17-Dynorphin A (swine)
154040-19-4	154396-74-4	154758-03-9
157932-94-0	158372-06-6	154974-44-4
		156790-69-1

RL: PRP (Properties)

(unclaimed sequence; protection of endogenous therapeutic peptides from
peptidase activity through conjugation to blood components)

IT	158561-91-2	158622-13-0	158879-51-7	158884-65-2	159623-45-7
	159829-06-8	159964-40-6	160112-12-9	160187-72-4	160210-00-4
	160507-34-6	161206-81-1	161748-27-2	162929-64-8	165338-06-7
	166546-45-8	166546-72-1	166824-48-2,	1-24-Neuropeptide Y (human)	
	167114-91-2	168633-88-3	169228-94-8,	Luteinizing hormone-releasing	
	factor (Sparus auratus)	170032-25-4	170032-27-6	170713-75-4,	
	Orphanin FQ (swine)	171089-50-2	171876-68-9	172838-27-6,	Protegrin 1
	(reduced)	172998-24-2,	16-36-Buforin I	174643-45-9	175799-54-9
	176260-88-1	176843-96-2	176843-98-4	178629-74-8	182374-54-5
	182804-15-5	183476-25-7	183788-96-7	185391-83-7	185391-85-9
	185458-37-1	185805-61-2	185805-76-9	186253-19-0	187345-00-2
	188405-30-3	188427-41-0	188954-16-7	189224-35-9	190436-05-6
	191280-45-2	191867-98-8	191919-78-5	191919-81-0	191919-84-3
	192432-73-8	195832-30-5	198276-46-9	198277-98-4	198333-83-4
	198481-81-1	198483-36-2	198483-37-3	198542-00-6	198623-87-9,
	1-16-Gastrin-releasing peptide (human)	198629-50-4	198757-82-3		
	198757-90-3	199847-29-5	200436-43-7	202063-45-4	209121-04-0
	209121-07-3	210889-41-1	211362-82-2	211362-85-5	211918-90-0
	213533-86-9	213768-42-4	215504-95-3	217449-42-8	218787-22-5
	220846-54-8	220997-11-5	221015-30-1	221102-52-9,	Uroguanylin (human
	reduced)	224825-60-9	239075-62-8	249284-54-6	251903-86-3
	252229-85-9	253316-46-0	253316-55-1	254747-93-8	254965-28-1
	256229-96-6	256229-97-7	256229-98-8	256230-19-0	256230-20-3
	256230-21-4	256230-22-5	256230-23-6	256230-24-7	256230-25-8
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	256230-32-7	256230-34-9	256933-30-9	259111-03-0	259243-44-2
	260060-44-4	260542-01-6	261962-20-3	263006-62-8	280748-65-4
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	308348-98-3	308348-99-4	308349-00-0	308349-01-1	308349-02-2
	308349-03-3	308349-04-4	308349-05-5	308349-06-6	308349-07-7
	308349-08-8	308349-09-9	308806-02-2	309243-70-7	309243-73-0
	309243-74-1	309243-75-2	309243-76-3	309243-77-4	309243-78-5
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	309244-40-4	309244-41-5	309244-42-6	309244-43-7	309244-44-8
	309244-45-9	309244-46-0	309244-47-1	309244-48-2	309244-49-3
	309244-50-6	309244-51-7	309244-52-8	309244-53-9	309244-54-0
	309244-55-1	309244-56-2	309244-57-3	309244-58-4	309244-59-5
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	309244-65-3	309244-66-4	309244-67-5	309244-68-6	309244-69-7
	309244-70-0	309244-71-1	309244-72-2	309244-87-9	309244-88-0

RL: PRP (Properties)

(unclaimed sequence; protection of endogenous therapeutic peptides from
peptidase activity through conjugation to blood components)

IT	309244-89-1	309244-90-4	309244-91-5	309244-92-6	309244-93-7
	309244-94-8	309244-95-9	309244-96-0	309244-97-1	309244-98-2
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	309245-09-8	309245-10-1	309245-11-2	309245-12-3	309245-13-4
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	309246-15-9	309246-16-0	309246-17-1	309246-18-2	309246-19-3
	309246-20-6	309246-21-7	309246-22-8	309246-24-0	309246-25-1
	309246-26-2	309246-27-3	309246-28-4	309246-29-5	309246-30-8
	309246-31-9	309246-32-0	309246-33-1	309246-34-2	309246-35-3
	309246-36-4	309246-37-5	309246-38-6	309246-39-7	309246-40-0
	309246-41-1	309246-42-2	309246-43-3	309246-44-4	309246-45-5
	309246-46-6	309246-47-7	309246-48-8	309246-49-9	309246-50-2
	309246-51-3	309246-52-4	309246-53-5	309246-54-6	309246-55-7
	309246-56-8	309246-57-9	309246-58-0	309246-59-1	309246-60-4
	309246-61-5	309246-62-6	309246-63-7	309246-64-8	309246-65-9
	309246-66-0	309246-67-1	309246-68-2	309246-69-3	309246-70-6
	309246-71-7	309246-72-8	309246-73-9	309246-74-0	309246-75-1
	309246-76-2	309246-77-3	309246-78-4	309246-79-5	309246-80-8
	309246-81-9	309246-82-0	309246-83-1	309246-84-2	309246-85-3
	309246-86-4	309246-87-5	309246-88-6	309246-89-7	309246-90-0
	309246-91-1	309246-92-2	309246-93-3	309246-94-4	309246-95-5
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	309247-12-9	309247-13-0	309247-14-1	309247-15-2	309247-16-3
	309247-17-4	309247-18-5	309247-19-6	309247-20-9	309247-21-0
	309247-22-1	309247-23-2	309247-24-3	309247-25-4	309247-26-5
	309247-27-6	309247-28-7	309247-29-8	309247-30-1	309247-31-2

RL: PRP (Properties)

(unclaimed sequence; protection of endogenous therapeutic peptides from
peptidase activity through conjugation to blood components)

IT	309247-32-3	309247-33-4	309247-34-5	309247-35-6	309247-36-7
	309247-37-8	309247-38-9	309247-39-0	309247-40-3	309247-41-4
	309247-42-5	309247-43-6	309247-44-7	309247-45-8	309247-46-9
	309247-47-0	309247-48-1	309247-49-2	309247-50-5	309247-51-6
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	309247-57-2	309247-58-3	309247-59-4	309247-60-7	309247-61-8
	309247-62-9	309247-63-0	309247-64-1	309247-65-2	309247-66-3
	309247-67-4	309247-68-5	309247-69-6	309247-70-9	309247-71-0
	309247-72-1	309247-73-2	309247-74-3	309247-75-4	309247-76-5

309247-77-6 309247-78-7 309247-80-1 309247-81-2 309247-82-3
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 309248-13-3 309248-14-4 309248-15-5 309248-16-6 309724-00-3

RL: PRP (Properties)

(unclaimed sequence; protection of endogenous therapeutic peptides from
 peptidase activity through conjugation to blood components)

L30 ANSWER 6 OF 11 HCAPLUS COPYRIGHT 2003 ACS on STN
 AN 2000:493318 HCAPLUS
 DN 133:129880
 ED Entered STN: 21 Jul 2000
 TI Methods using an exendin or related substance for glucagon suppression
 IN Young, Andrew; Gedulin, Bronislava
 PA Amylin Pharmaceuticals, Inc., USA
 SO PCT Int. Appl., 96 pp.
 CODEN: PIXXD2
 DT Patent
 LA English
 IC A61K038-26
 CC 1-10 (Pharmacology)
 FAN.CNT 4

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2000041548	A2	20000720	WO 2000-US942	20000114 <--
	WO 2000041548	A3	20001130		
	W:	AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
	RW:	GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG			
	CA 2356331	AA	20000720	CA 2000-2356331	20000114 <--
	EP 1143989	A2	20011017	EP 2000-902415	20000114 <--
	EP 1143989	A3	20020911		
	R:	AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO			
	BR 2000007823	A	20011120	BR 2000-7823	20000114 <--
	JP 2002538084	T2	20021112	JP 2000-593169	20000114 <--
	NO 2001003469	A	20010914	NO 2001-3469	20010712 <--
PRAI	US 1999-116380P	P	19990114	<--	
	US 1999-132017P	P	19990430	<--	
	US 2000-175365P	P	20000110		
	WO 2000-US942	W	20000114	<--	
AB	Methods are provided for use of an exendin, an exendin agonist, or a modified exendin or exendin agonist having an exendin or exendin agonist linked to one or more polyethylene glycol polymers, for example, for lowering glucagon levels and/or suppressing glucagon secretion in a subject. These methods are useful in treating hyperglucagonemia and other conditions that would be benefited by lowering plasma glucagon or suppressing glucagon secretion.				
ST	exendin glucagon suppression; hyperglucagonemia glucagon suppression exendin				
IT	Kidney				
	(clearance by; exendin or related substance for glucagon suppression)				
IT	Polyoxyalkylenes, biological studies				

RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)

(exendin conjugates; exendin or related substance for glucagon suppression)

IT Antidiabetic agents

Gastric emptying

(exendin or related substance for glucagon suppression)

IT Pancreatic islet of Langerhans

Pancreatic islet of Langerhans

(glucagonoma, inhibitors; exendin or related substance for glucagon suppression)

IT Antitumor agents

(glucagonoma; exendin or related substance for glucagon suppression)

IT Erythema

(necrolytic migratory; exendin or related substance for glucagon suppression)

IT Diabetes mellitus

(non-insulin-dependent; exendin or related substance for glucagon suppression)

IT 130357-25-4P, Exendin 3 (Heloderma horridum) 141758-74-9P, Exendin 4 (Heloderma suspectum)

RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); PRP (Properties); SPN (Synthetic preparation); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)

(exendin or related substance for glucagon suppression)

IT 25322-68-3D, Polyethylene glycol, exendin conjugates 141732-76-5, Exendin 4 213190-65-9, Exendin 213190-65-9D, Exendin, derivs.

RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)

(exendin or related substance for glucagon suppression)

IT 50-99-7, D-Glucose, biological studies 9007-92-5, Glucagon, biological studies

RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)

(exendin or related substance for glucagon suppression)

IT 141758-74-9, Exendin 4 (Heloderma suspectum) 284676-24-0

285575-19-1 285575-20-4 286009-27-6 286009-36-7 286009-39-0
286009-44-7 286009-59-4 286369-25-3 286369-29-7 286369-35-5
286369-36-6 286369-37-7 286369-39-9 286369-40-2 286369-41-3
286369-42-4 286369-43-5

RL: PRP (Properties)

(unclaimed protein sequence; methods using an exendin or related substance for glucagon suppression)

IT 285575-21-5

RL: PRP (Properties)

(unclaimed protein sequence; methods using an exendin or related substance for glucagon suppression)

IT 285988-95-6

RL: PRP (Properties)

(unclaimed sequence; 7 methods using an exendin or related substance for glucagon suppression)

IT 210712-28-0, 1-30-Exendin 4 (Heloderma suspectum) 210712-29-1

210712-30-4 210712-31-5 210712-33-7 210712-34-8 210712-37-1
210712-38-2 210712-39-3 210712-40-6 210712-41-7 210712-42-8
210712-44-0 210712-45-1 210712-46-2 210712-47-3 210712-48-4
210712-49-5 210712-50-8 210712-51-9 210712-52-0 210712-53-1
210712-54-2 210712-55-3 210712-56-4 210712-57-5 210712-58-6
210712-59-7 210712-60-0 210712-61-1 210712-62-2 210712-69-9
210712-71-3 210712-72-4 210712-73-5 210712-74-6 210712-75-7
210712-76-8 210712-77-9 210712-78-0 210712-79-1 210712-80-4

210712-81-5	210712-82-6	210712-83-7	210712-84-8	210712-86-0
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210712-96-2	210712-97-3	210712-98-4	210712-99-5	210713-00-1
210713-02-3	210713-03-4	210713-06-7	210713-07-8	210713-08-9
210713-09-0	210713-10-3	210713-11-4	210713-12-5	210713-13-6
210713-16-9	210713-18-1	210713-19-2	210713-22-7	210713-23-8
210713-24-9	210713-25-0	210713-27-2	210713-28-3	210713-29-4
210713-31-8	210713-33-0	210713-35-2	210713-36-3	210713-37-4
210713-38-5	210713-39-6	210824-13-8	210824-35-4	210824-60-5
210824-78-5	210824-96-7	210824-97-8	210825-12-0	210828-28-7
210828-38-9	210828-91-4	210828-92-5	210829-01-9	210829-03-1
210829-35-9	210829-39-3	210829-43-9	210829-44-0	210829-45-1
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285554-92-9	285554-94-1	285554-96-3	285554-98-5	285555-00-2
285555-02-4	285555-04-6	285555-09-1	285555-11-5	285555-19-3
285555-30-8	285555-31-9	285555-32-0	285555-33-1	285555-34-2
285555-37-5	285555-40-0	285555-43-3	285555-44-4	285575-22-6
285575-23-7	285575-24-8	285575-25-9	285575-26-0	285575-27-1
285575-28-2	285575-29-3	285575-30-6	285575-31-7	285988-69-4
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285988-94-5	286369-45-7			

RL: PRP (Properties)

(unclaimed sequence; methods using an exendin or related substance for glucagon suppression)

L30 ANSWER 7 OF 11 HCAPLUS COPYRIGHT 2003 ACS on STN

AN 2000:493315 HCAPLUS

DN 133:135612

ED Entered STN: 21 Jul 2000

TI Novel exendin agonist formulations and methods of administration thereof

IN Young, Andrew; L'Italien, James J.; Kolterman, Orville

PA Amylin Pharmaceuticals, Inc., USA

SO PCT Int. Appl., 281 pp.

CODEN: PIXXD2

DT Patent

LA English

IC A61K038-16

CC 34-3 (Amino Acids, Peptides, and Proteins)

Section cross-reference(s): 2, 63

FAN.CNT 4

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2000041546	A2	20000720	WO 2000-US902	20000114 <--
	W:	AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
	RW:	GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG			
	CA 2356706	AA	20000720	CA 2000-2356706	20000114 <--
	EP 1140145	A2	20011010	EP 2000-914425	20000114 <--
	R:	AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO			
	BR 2000007820	A	20011120	BR 2000-7820	20000114 <--
	JP 2002534450	T2	20021015	JP 2000-593167	20000114 <--
	NO 2001003468	A	20010914	NO 2001-3468	20010712 <--
	US 2003087820	A1	20030508	US 2002-157224	20020528 <--
PRAI	US 1999-116380P	P	19990114 <--		
	US 2000-175365P	P	20000110		

WO 2000-US902 W 20000114

US 2001-889330 A2 20011227

- AB Novel exendin and exendin agonist compound formulations and dosages and methods of administration thereof are provided. These compns. and methods are useful in treating diabetes and conditions that would be benefited by lowering plasma glucose or delaying and/or slowing gastric emptying or inhibiting food intake.
- ST exendin agonist antidiabetic sequence appetite suppressant
- IT Glucagon-like peptide-1 receptors
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(GLP-1; novel exendin agonist formulations and methods of administration thereof as antidiabetic agents and appetite suppressants)
- IT Buffers
(acetate; novel exendin agonist formulations and methods of administration thereof as antidiabetic agents and appetite suppressants)
- IT Drug delivery systems
(buccal; novel exendin agonist formulations and methods of administration thereof as antidiabetic agents and appetite suppressants)
- IT Phosphates, uses
RL: NUU (Other use, unclassified); USES (Uses)
(buffers; novel exendin agonist formulations and methods of administration thereof as antidiabetic agents and appetite suppressants)
- IT Stomach
(emptying of; novel exendin agonist formulations and methods of administration thereof as antidiabetic agents and appetite suppressants)
- IT Drug delivery systems
(freeze-dried; novel exendin agonist formulations and methods of administration thereof as antidiabetic agents and appetite suppressants)
- IT Drug delivery systems
(injections, s.c.; novel exendin agonist formulations and methods of administration thereof as antidiabetic agents and appetite suppressants)
- IT Drug delivery systems
(injections; novel exendin agonist formulations and methods of administration thereof as antidiabetic agents and appetite suppressants)
- IT Drug delivery systems
(intratracheal; novel exendin agonist formulations and methods of administration thereof as antidiabetic agents and appetite suppressants)
- IT Polyoxyalkylenes, uses
RL: NUU (Other use, unclassified); USES (Uses)
(iso-osmolality modifier; novel exendin agonist formulations and methods of administration thereof as antidiabetic agents and appetite suppressants)
- IT Solutions
(isotonic solns.; novel exendin agonist formulations and methods of administration thereof as antidiabetic agents and appetite suppressants)
- IT Drug delivery systems
(liqs.; novel exendin agonist formulations and methods of administration thereof as antidiabetic agents and appetite suppressants)
- IT Osmolality
(modifiers; novel exendin agonist formulations and methods of administration thereof as antidiabetic agents and appetite suppressants)

- suppressants)
- IT Drug delivery systems
(nasal; novel exendin agonist formulations and methods of administration thereof as antidiabetic agents and appetite suppressants)
- IT Diabetes mellitus
(non-insulin-dependent; novel exendin agonist formulations and methods of administration thereof as antidiabetic agents and appetite suppressants)
- IT Detergents
(nonionic; novel exendin agonist formulations and methods of administration thereof as antidiabetic agents and appetite suppressants)
- IT Antidiabetic agents
Appetite depressants
Heloderma horridum
Heloderma suspectum
Obesity
Physiological saline solutions
Preservatives
Protein sequences
Surfactants
Thickening agents
pH
(novel exendin agonist formulations and methods of administration thereof as antidiabetic agents and appetite suppressants)
- IT Peptides, preparation
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); PRP (Properties); SPN (Synthetic preparation); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(novel exendin agonist formulations and methods of administration thereof as antidiabetic agents and appetite suppressants)
- IT Drug delivery systems
(oral; novel exendin agonist formulations and methods of administration thereof as antidiabetic agents and appetite suppressants)
- IT Drug delivery systems
(parenterals; novel exendin agonist formulations and methods of administration thereof as antidiabetic agents and appetite suppressants)
- IT Alcohols, uses
RL: NUU (Other use, unclassified); USES (Uses)
(polyhydric, iso-osmolality modifiers; novel exendin agonist formulations and methods of administration thereof as antidiabetic agents and appetite suppressants)
- IT Drug delivery systems
(pulmonary; novel exendin agonist formulations and methods of administration thereof as antidiabetic agents and appetite suppressants)
- IT Drug delivery systems
(sublingual; novel exendin agonist formulations and methods of administration thereof as antidiabetic agents and appetite suppressants)
- IT 107444-51-9P 130357-25-4P, Exendin-3 (Heloderma horridum)
141758-74-9P, Exendin-4 (Heloderma suspectum) 210712-28-0P, 1-30-Exendin 4 (Heloderma suspectum) 210712-29-1P 210712-30-4P 210712-31-5P
210712-33-7P 210712-35-9P 210712-36-0P 210712-37-1P 210712-38-2P
210712-39-3P 210712-40-6P 210712-41-7P 210712-42-8P 210712-43-9P
210712-44-0P 210712-45-1P 210712-46-2P 210712-47-3P 210712-48-4P
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210712-54-2P 210712-55-3P 210712-56-4P 210712-57-5P 210712-58-6P
210712-59-7P 210712-60-0P 210712-61-1P 210712-62-2P 210712-63-3P
210712-64-4P 210712-65-5P 210712-67-7P 210712-68-8P 210712-69-9P

210712-70-2P	210712-71-3P	210712-72-4P	210712-73-5P	210712-74-6P
210712-75-7P	210712-76-8P	210712-77-9P	210712-78-0P	210712-79-1P
210712-80-4P	210712-81-5P	210712-82-6P	210712-83-7P	210712-84-8P
210712-85-9P	210712-86-0P	210712-87-1P	210712-88-2P	210712-89-3P
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210713-00-1P	210713-01-2P	210713-02-3P	210713-03-4P	210713-04-5P
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210713-37-4P	210713-38-5P	210713-39-6P	210753-27-8P	210753-40-5P
210753-41-6P	210753-42-7P	210753-43-8P	210753-44-9P	210824-13-8P
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210825-12-0P	210828-28-7P	210828-38-9P	210828-61-8P	210828-91-4P
210828-92-5P	210828-93-6P	210829-01-9P	210829-02-0P	210829-03-1P
210829-04-2P	210829-07-5P	210829-08-6P	210829-10-0P	210829-11-1P
210829-12-2P	210829-35-9P	210829-36-0P	210829-38-2P	210829-39-3P
210829-43-9P	210829-44-0P	210829-45-1P	210829-52-0P	210829-53-1P
210829-57-5P	210829-60-0P	210829-61-1P	238091-55-9P	239091-09-9P
284676-24-0P	284685-04-7P	284685-05-8P		

RL: BAC (Biological activity or effector, except adverse); BOC (Biological occurrence); BSU (Biological study, unclassified); PNU (Preparation, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); PREP (Preparation); USES (Uses)

(amino acid sequence; novel exendin agonist formulations and methods of administration thereof as antidiabetic agents and appetite suppressants)

IT 50-99-7, D-Glucose, biological studies

RL: BOC (Biological occurrence); BSU (Biological study, unclassified); BIOL (Biological study); OCCU (Occurrence)

(blood; novel exendin agonist formulations and methods of administration thereof as antidiabetic agents and appetite suppressants)

IT 126-44-3, Citrate, uses 11070-68-1, Glutamate, uses

RL: NUU (Other use, unclassified); USES (Uses)

(buffers; novel exendin agonist formulations and methods of administration thereof as antidiabetic agents and appetite suppressants)

IT 71-50-1, Acetate, properties

RL: NUU (Other use, unclassified); PEP (Physical, engineering or chemical process); PRP (Properties); PROC (Process); USES (Uses)

(buffers; novel exendin agonist formulations and methods of administration thereof as antidiabetic agents and appetite suppressants)

IT 50-70-4, Sorbitol, uses 56-81-5, 1,2,3-Propanetriol, uses 59-23-4, Galactose, uses 69-65-8, Mannitol 87-89-8, Inositol 87-99-0, Xylitol 25322-68-3

RL: NUU (Other use, unclassified); USES (Uses)

(iso-osmolality modifier; novel exendin agonist formulations and methods of administration thereof as antidiabetic agents and appetite suppressants)

IT 213190-65-9P, Exendin

RL: BAC (Biological activity or effector, except adverse); BOC (Biological occurrence); BPN (Biosynthetic preparation); BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); PREP (Preparation); USES (Uses)

(novel exendin agonist formulations and methods of administration thereof as antidiabetic agents and appetite suppressants)

IT 89750-14-1, Glucagon-like peptide I

RL: BAC (Biological activity or effector, except adverse); BSU (Biological

study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
 (novel exendin agonist formulations and methods of administration thereof as antidiabetic agents and appetite suppressants)

IT 63-42-3 147-81-9, Arabinose 9005-65-6, Polysorbate 80
 RL: NUU (Other use, unclassified); USES (Uses)
 (novel exendin agonist formulations and methods of administration thereof as antidiabetic agents and appetite suppressants)

IT 94-13-3, Propyl paraben 94-26-8, Butyl paraben 99-76-3, Methyl paraben 100-51-6, Benzenemethanol, biological studies 108-39-4, biological studies 108-95-2, Phenol, biological studies 120-47-8, Ethyl paraben
 RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); PEP (Physical, engineering or chemical process); THU (Therapeutic use); BIOL (Biological study); PROC (Process); USES (Uses)
 (preservative; novel exendin agonist formulations and methods of administration thereof as antidiabetic agents and appetite suppressants)

IT 9004-10-8, Insulin, biological studies
 RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); BIOL (Biological study)
 (sensitivity to; novel exendin agonist formulations and methods of administration thereof as antidiabetic agents and appetite suppressants)

IT 285991-14-2
 RL: PRP (Properties)
 (unclaimed protein sequence; novel exendin agonist formulations and methods of administration thereof)

L30 ANSWER 8 OF 11 HCAPLUS COPYRIGHT 2003 ACS on STN

AN 1998:550504 HCAPLUS

DN 129:185369

ED Entered STN: 31 Aug 1998

TI Polynucleotides encoding proexendin, and methods and uses thereof

IN Drucker, Daniel J.

PA 1149336 Ontario Inc., Can.

SO PCT Int. Appl., 27 pp.

CODEN: PIXXD2

DT Patent

LA English

IC ICM C12N015-12

ICS C12N015-11; C07K014-575; C07K016-18

CC 4-5 (Toxicology)

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE	
PI	WO 9835033	A1	19980813	WO 1998-CA71	19980204	<--
	W:	AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZW, AM, AZ, EY, KG, KZ, MD, RU, TJ, TM				
	RW:	GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
	AU 9858507	A1	19980826	AU 1998-58507	19980204	<--
	EP 981611	A1	20000301	EP 1998-901908	19980204	<--
	R:	AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
	JP 2001512307	T2	20010821	JP 1998-533455	19980204	<--
PRAI	US 1997-37412P	P	19970205			<--
	GB 1997-2582	A	19970207			<--
	WO 1998-CA71	W	19980204			<--
AB	Exendin 4 is a biol. active peptide first isolated from Gila monster					

venom. The invention encompasses polynucleotides encoding proexendin peptides, including exendin and novel peptides, as well as isolated or recombinant proexendin peptides. The invention also includes antibodies which specifically recognize such peptides.

ST Heloderma proexendin sequence immunity insulinotropic diabetes
 IT Immunity
 (administration of peptides for immunity; gene encoding proexendin from Heloderma horridum and applications)
 IT Heloderma horridum
 Protein sequences
 (gene encoding proexendin from Heloderma horridum and applications)
 IT Antibodies
 RL: ARU (Analytical role, unclassified); BSU (Biological study, unclassified); ANST (Analytical study); BIOL (Biological study)
 (gene encoding proexendin from Heloderma horridum and applications)
 IT Diabetes mellitus
 (non-insulin-dependent, insulinotropic GLP-1 like properties of exendin with applications for treatment of diabetes; gene encoding proexendin from Heloderma horridum and applications)
 IT 141732-76-5, Exendin 4
 RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
 (alternative form of;; gene encoding proexendin from Heloderma horridum and applications)
 IT 211430-73-8, Exendin ENTP (Heloderma horridum)
 RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
 (amino acid sequence of mature; gene encoding proexendin from Heloderma horridum and applications)
 IT 188265-76-1, Exendin 4, pro- (Heloderma suspectum) 203743-40-2
 211319-01-6 211319-02-7 211319-03-8 **211430-62-5**
 211430-68-1, 1-47-Exendin ENTP (Heloderma horridum)
 RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
 (amino acid sequence; gene encoding proexendin from Heloderma horridum and applications)
 IT 89750-14-1, Glucagon-like peptide I
 RL: BSU (Biological study, unclassified); BIOL (Biological study)
 (insulinotropic GLP-1 like properties of exendin with applications for treatment of diabetes; gene encoding proexendin from Heloderma horridum and applications)
 IT 211621-97-5
 RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
 (nucleotide sequence; gene encoding proexendin from Heloderma horridum and applications)

RE.CNT 4 THERE ARE 4 CITED REFERENCES AVAILABLE FOR THIS RECORD

RE

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- (2) Eng, J; US 5424286 A 1995 HCAPLUS
- (3) Eng, J; JOURNAL OF BIOLOGICAL CHEMISTRY 1992, V267(11), P7402 HCAPLUS
- (4) Pohl, M; GASTROENTEROLOGY, SUPPLEMENT 1997, V112(4), PA1181

L30 ANSWER 9 OF 11 HCAPLUS COPYRIGHT 2003 ACS on STN

AN 1998:490528 HCAPLUS

DN 129:149256

ED Entered STN: 06 Aug 1998

TI Preparation of exendin peptides for the reduction of food intake

IN Beeley, Nigel Robert Arnold; Prickett, Kathryn S.; Bhavsar, Sunil

PA **Amylin Pharmaceuticals, Inc., USA**

SO PCT Int. Appl., 214 pp.

CODEN: PIXXD2

DT Patent

LA English
 IC ICM A61K038-16
 CC 34-3 (Amino Acids, Peptides, and Proteins)
 Section cross-reference(s): 1, 17

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9830231	A1	19980716	WO 1998-US449	19980107 <--
	W:	AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
	RW:	GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG			
	AU 9862394	A1	19980803	AU 1998-62394	19980107 <--
	AU 739020	B2	20011004		
	EP 996459	A1	20000503	EP 1998-904545	19980107 <--
	R:	AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI			
	JP 2002508742	T2	20020319	JP 1998-531147	19980107 <--
	US 2002137666	A1	20020926	US 1998-3869	19980107 <--
	WO 9907404	A1	19990218	WO 1998-US16387	19980806 <--
	W:	AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
	RW:	GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG			
	AU 9887729	A1	19990301	AU 1998-87729	19980806 <--
	AU 749914	B2	20020704		
	EP 1019077	A1	20000719	EP 1998-939260	19980806 <--
	R:	AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI			
	BR 9811866	A	20000815	BR 1998-11866	19980806 <--
	JP 2001513512	T2	20010904	JP 2000-506993	19980806 <--
	CA 2309356	AA	19990527	CA 1998-2309356	19981113 <--
	CA 2310097	AA	19990527	CA 1998-2310097	19981113 <--
	WO 9925727	A2	19990527	WO 1998-US24210	19981113 <--
	W:	AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
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	WO 9925728	A1	19990527	WO 1998-US24273	19981113 <--
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	AU 9914046	A1	19990607	AU 1999-14046	19981113 <--
	AU 757748	B2	20030306		
	AU 9914588	A1	19990607	AU 1999-14588	19981113 <--
	AU 756836	B2	20030123		

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 R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,
 IE, FI

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 R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,
 IE, FI

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 NZ 504258 A 20021220 NZ 1998-504258 19981113 <--
 NZ 504256 A 20030131 NZ 1998-504256 19981113 <--
 JP 2003522721 T2 20030729 JP 2000-521107 19981113 <--
 US 2003087821 A1 20030508 US 2002-187051 20020628 <--

PRAI US 1997-34905P P 19970107 <--
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 WO 1998-US24273 W 19981113 <--

AB Methods for treating conditions or disorders which can be alleviated by
 reducing food intake are disclosed which comprise administration of an
 effective amount of an exendin or an exendin agonist, alone or in
 conjunction with other compds. or compns. that effect satiety. Approx.
 180 exendin-related peptides were synthesized by the solid-phase method.

ST exendin peptide prepn redn food intake

IT Appetite
 (disorder; preparation of exendin peptides for the reduction of food intake)

IT Appetite depressants
 Feeding
 (preparation of exendin peptides for the reduction of food intake)

IT Peptides, preparation
 RL: FFD (Food or feed use); SPN (Synthetic preparation); BIOL (Biological
 study); PREP (Preparation); USES (Uses)
 (preparation of exendin peptides for the reduction of food intake)

IT 210712-52-0P
 RL: FFD (Food or feed use); SPN (Synthetic preparation); BIOL (Biological
 study); PREP (Preparation); USES (Uses)
 (.preparation of exendin peptides for the reduction of food intake)

IT 158345-16-5P 203743-29-7P 203743-31-1P
 203743-32-2P 203743-33-3P 203743-35-5P
 203743-36-6P 203743-37-7P 203743-38-8P
 203743-39-9P 203743-40-2P 203743-41-3P
 203743-45-7P 203743-46-8P 203743-47-9P
 203743-50-4P 203743-53-7P 203743-54-8P 210712-28-0P,
 1-30-Exendin 4 (Heloderma suspectum) 210712-29-1P 210712-30-4P
 210712-31-5P 210712-32-6P 210712-33-7P 210712-34-8P 210712-35-9P
 210712-36-0P 210712-37-1P 210712-38-2P 210712-39-3P 210712-40-6P
 210712-41-7P 210712-42-8P 210712-43-9P 210712-44-0P 210712-45-1P
 210712-46-2P 210712-47-3P 210712-48-4P 210712-49-5P 210712-50-8P
 210712-51-9P 210712-53-1P 210712-54-2P 210712-55-3P 210712-56-4P
 210712-57-5P 210712-58-6P 210712-59-7P 210712-60-0P 210712-61-1P
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 210712-67-7P 210712-68-8P 210712-69-9P 210712-70-2P 210712-71-3P
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 210712-77-9P 210712-78-0P 210712-79-1P 210712-80-4P 210712-81-5P
 210712-82-6P 210712-83-7P 210712-84-8P 210712-85-9P 210712-86-0P
 210712-87-1P 210712-88-2P 210712-89-3P 210712-90-6P 210712-91-7P
 210712-92-8P 210712-93-9P 210712-94-0P 210712-95-1P 210712-96-2P
 210712-97-3P 210712-98-4P 210712-99-5P 210713-00-1P 210713-01-2P
 210713-02-3P 210713-03-4P 210713-04-5P 210713-05-6P 210713-06-7P

210713-07-8P 210713-08-9P 210713-09-0P 210713-10-3P 210713-11-4P
 210713-12-5P 210713-13-6P 210713-14-7P 210713-15-8P 210713-16-9P
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 210713-22-7P 210713-23-8P 210713-24-9P 210713-25-0P 210713-26-1P
 210713-27-2P 210713-28-3P 210713-29-4P 210713-30-7P 210713-31-8P
 210713-33-0P 210713-35-2P 210713-36-3P 210713-37-4P 210713-38-5P
 210713-39-6P 210753-27-8P 210753-40-5P 210753-41-6P 210753-42-7P
 210753-43-8P 210753-44-9P 210824-13-8P 210824-14-9P 210824-35-4P
 210824-60-5P 210824-78-5P 210824-96-7P 210824-97-8P 210825-12-0P
 210828-28-7P 210828-38-9P 210828-61-8P 210828-91-4P 210828-92-5P
 210828-93-6P 210829-01-9P 210829-02-0P 210829-03-1P 210829-04-2P
 210829-07-5P 210829-08-6P 210829-09-7P 210829-10-0P 210829-11-1P
 210829-12-2P 210829-35-9P 210829-36-0P 210829-38-2P 210829-39-3P
 210829-41-7P 210829-43-9P 210829-44-0P 210829-45-1P
 210829-46-2P 210829-52-0P 210829-53-1P 210829-56-4P
 210829-57-5P 210829-59-7P 210829-60-0P 210829-61-1P
 210830-02-7P 210830-13-0P 210830-14-1P 210830-15-2P
 210830-22-1P 210830-29-8P 210830-31-2P 210830-35-6P
 210830-59-4P

RL: FFD (Food or feed use); SPN (Synthetic preparation); BIOL (Biological study); PREP (Preparation); USES (Uses)

(preparation of exendin peptides for the reduction of food intake)

RE.CNT 1 THERE ARE 1 CITED REFERENCES AVAILABLE FOR THIS RECORD

RE

(1) Eng; US 5424286 A 1995 HCAPLUS

L30 ANSWER 10 OF 11 HCAPLUS COPYRIGHT 2003 ACS on STN

AN 1998:112250 HCAPLUS

DN 128:192936

ED Entered STN: 25 Feb 1998

TI Preparation of exendin peptide analogs as agonists for regulating gastrointestinal motility

IN Young, Andrew A.; Gedulin, Bronislava; Beeley, Nigel
 Robert Arnold; Prickett, Kathryn S.

PA Amylin Pharmaceuticals, Inc., USA; Young, Andrew A.; Gedulin,
 Bronislava; Beeley, Nigel Robert Arnold; Prickett, Kathryn S.

SO PCT Int. Appl., 70 pp.

CODEN: PIXXD2

DT Patent

LA English

IC ICM A61K038-00

ICS A61K038-26; G03F005-00; C07K002-00; C07K005-00

CC 34-3 (Amino Acids, Peptides, and Proteins)

Section cross-reference(s): 1

FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9805351	A1	19980212	WO 1997-US14199	19970808 <--
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM RW: GH, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
AU 9740636	A1	19980225	AU 1997-40636	19970808 <--
EP 966297	A1	19991229	EP 1997-938261	19970808 <--
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
JP 2001501593	T2	20010206	JP 1998-508263	19970808 <--
PRAI US 1996-694954	A	19960808	<--	
WO 1997-US14199	W	19970808	<--	

OS MARPAT 128:192936

AB Methods for reducing gastric motility and delaying gastric emptying for therapeutic and diagnostic purposes are disclosed which comprise administration of an effective amount of an exendin or an exendin agonist H-Xaa1-Xaa2-Xaa3-Gly-Thr-Xaa4-Xaa5-Xaa6-Xaa7-Xaa8-Ser-Lys-Gln-Xaa9-Glu-Glu-Glu-Ala-Val-Arg-Leu-Xaa10-Xaa11-Xaa12-Xaa13-Leu-Lys-Asn-Gly-Gly-Xaa14-Ser-Ser-Gly-Ala-Xaa15-Xaa16-Xaa17-Xaa18-Z [Xaa1 = His, Arg, Tyr; Xaa2 = Ser, Gly, Ala, Thr; Xaa3, Xaa7, Xaa12 = independently Asp, Glu; Xaa4, Xaa10 = independently Phe, Tyr, naphthylalanine; Xaa5, Xaa6 = independently Thr, Ser; Xaa8, Xaa9 = independently Leu, Ile, Val, pentylglycine, Met; Xaa11 = any group Xaa8, tert-butylglycine; Xaa13 = any group Xaa4, Trp; Xaa14-Xaa17 = independently Pro, homoproline, 3-Hyp, 4-Hyp, thioproline, N-alkylglycine, N-alkylpentylglycine, N-alkylalanine; Xaa18 = Ser, Thr, Tyr; Z = OH, NH₂; with the proviso that the compound does not have the formula of exendin-3 or exendin-4] or a pharmaceutically acceptable salt thereof. Methods for treating conditions associated with elevated, inappropriate, or undesired post-prandial blood glucose levels are disclosed which comprise administration of an effective amount of an exendin or an exendin agonist alone or in conjunction with other anti-gastric emptying agents. Thus, exendin-4 acid and [Leu14,Phe25]-exendin-4, prepared by standard solid-phase methods on a 4-(2,4-dimethoxyphenyl)-Fmoc-aminomethylphenoxyacetamide norleucine-MBHA resin using 9-fluorenylmethoxycarbonyl (Fmoc)-protected amino acids, inhibited gastric emptying in male HSD rats with EC₅₀ = 0.12 and 0.29 µg. Exendin-4 showed EC₅₀ = 0.27 µg under the same conditions.

ST exendin analog prepn gastrointestinal motility antagonist; gastric emptying antagonist exendin analog prepn; antidiabetic agent exendin analog prepn

IT Antidiabetic agents
Gastric emptying
Gastrointestinal motility
(preparation of exendin peptide analogs as agonists for regulating gastrointestinal motility)

IT 107444-51-9P, Glucagon-like peptide-I(7-36) amide 130357-25-4P, Exendin-3 (Heloderma horridum) 133514-43-9P, Exendin[9-39] 141758-74-9P, Exendin-4 (Heloderma suspectum) 158345-16-5P
203743-26-4P 203743-27-5P 203743-28-6P
203743-29-7P 203743-30-0P 203743-31-1P
203743-32-2P 203743-33-3P 203743-35-5P
203743-36-6P 203743-37-7P 203743-38-8P
203743-39-9P 203743-40-2P 203743-41-3P 203743-42-4P
203743-43-5P 203743-44-6P 203743-45-7P
203743-46-8P 203743-47-9P 203743-48-0P 203743-49-1P
203743-50-4P 203743-51-5P 203743-52-6P
203743-53-7P 203743-54-8P 203743-55-9P
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); SPN (Synthetic preparation); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(preparation of exendin peptide analogs as agonists for regulating gastrointestinal motility)

RE.CNT 12 THERE ARE 12 CITED REFERENCES AVAILABLE FOR THIS RECORD

RE

- (1) Amylin Pharmaceuticals Inc; WO 9507098 1995
- (2) Bayer; Clinical Chemistry 1996, V42(8B), P1361
- (3) Chernish; US 3862301 A 1973 HCAPLUS
- (4) Daniel; Br Med J 1974, V3, P720 MEDLINE
- (5) Dupre; Diabetes 1995, V44(6), P626 HCAPLUS
- (6) D'Alessio; J Clin Invest 1994, V93(5), P2263 HCAPLUS
- (7) Hellstrom; Scand J Gastroenterol 1993, V28(Suppl 197), P38
- (8) Miholic; Chirurgisches Forum 1991, P429 HCAPLUS
- (9) Nauck; Diabetologia, Abstract No 148 1995, V38(Suppl 1), PA39
- (10) Rai; Am Physiol J 1993, V265, PG118 MEDLINE
- (11) Schirra; Gastroenterology 1995, V108(4), PA1003

- (12) Schirra; Proceedings of the Association of American Physicians 1997,
V109(1), P84 HCAPLUS

L30 ANSWER 11 OF 11 HCAPLUS COPYRIGHT 2003 ACS on STN
 AN 1994:622490 HCAPLUS
 DN 121:222490
 ED Entered STN: 12 Nov 1994
 TI Use of 125I-[Y39]exendin-4 to characterize exendin receptors on dispersed
 pancreatic acini and gastric chief cells from guinea pig
 AU Singh, Gurcharn; Eng, John; Raufman, Jean-Pierre
 CS Gastrointestinal Cell Biology Laboratory, State University of New
 York-Health Science Center at Brooklyn, 450 Clarkson Avenue-Box 1196,
 Brooklyn, NY, 11203-2098, USA
 SO Regulatory Peptides (1994), 53(1), 47-59
 CODEN: REPPDY; ISSN: 0167-0115
 DT Journal
 LA English
 CC 2-6 (Mammalian Hormones)
 AB We synthesized and iodinated an exendin-4 analog, [Y39]exendin-4 (700
 Ci/mmol), for use as a radioligand to characterize exendin receptors on
 dispersed pancreatic acini and gastric chief cells from guinea pig.
 Binding of this bioactive radioligand was rapid, temperature-dependent and
 specific (not inhibited by other pancreatic or gastric secretagogues).
 Measurement of the ability of exendin-4 to inhibit the binding of
 125I-[Y39]exendin-4 indicated the presence of two classes of receptors.
 Pancreatic acini had 12.5 + 1010 binding sites/mg acinar protein of
 which 6% were high affinity ($K_d = 0.5$ nM) and 94% were low affinity ($K_d =$
 0.1 μ M). Chief cells had 3370 binding sites/cell of which 9% were high
 affinity ($K_d = 0.3$ nM) and 91% were low affinity ($K_d = 0.2$ μ M).
 Washing with 0.2 M acetic acid (pH 2.5), 0.2 M glycine (pH 10.5), or
 trypsin (100 μ g/mL) after 30 min incubation at 37°, indicated
 that 63 and 49% of radioligand was internalized in acini and chief cells,
 resp. Truncated glucagon-like peptide-1 (tGLP-1), a mammalian peptide
 sharing 53% homol. with exendin-4, inhibited radioligand binding at the
 same concns. that altered secretion from acini and chief cells. Glucagon,
 GLP-1 and GLP-2 inhibited 125I-[Y39]exendin-4 binding only at concns.
 ≥ 100 nM. Exendin(9-39)NH₂, a specific exendin-receptor antagonist,
 potently inhibited 125I-[Y39] exendin-4 binding ($IC_{50} = 6.1$ and 3.5 nM in
 acini and chief cells, resp.). In pancreatic acini and gastric chief
 cells from guinea pig, exendin-3, exendin-4 and tGLP-1 increase cellular
 cAMP and modulate enzyme secretion by interacting with high-affinity
 exendin receptors. 125I-[Y39] exendin-4 is a useful radioligand for
 studying exendin receptors.
 ST exendin receptor pancreas stomach
 IT Enzymes
 RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL
 (Biological study); PROC (Process)
 (exendins modulation of pancreas acinus and stomach chief cell
 secretion of)
 IT Pancreas
 (acinus, exendin receptors of)
 IT Stomach
 (chief cell, exendin receptors of)
 IT Receptors
 RL: BAC (Biological activity or effector, except adverse); BPR (Biological
 process); BSU (Biological study, unclassified); BIOL (Biological study);
 PROC (Process)
 (exendin, of pancreas acini and stomach chief cells)
 IT 118549-37-4, Insulinotropin 130357-25-4, Exendin 3 (Heloderma horridum)
 141758-74-9
 RL: BAC (Biological activity or effector, except adverse); BSU (Biological
 study, unclassified); BIOL (Biological study)
 (cAMP formation and enzyme secretion by pancreas acinus and stomach

chief cells response to)

IT 60-92-4, CAMP
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(exendins modulation of pancreas acinus and stomach chief cell formation of)

IT 158345-16-5P
RL: RCT (Reactant); SPN (Synthetic preparation); PREP (Preparation); RACT (Reactant or reagent)
(preparation and radioiodination of)

IT 158345-15-4P 158345-17-6P
RL: SPN (Synthetic preparation); PREP (Preparation)
(preparation as radioligand for extendin receptors)

=> fil uspatall

FILE 'USPATFULL' ENTERED AT 10:17:55 ON 29 DEC 2003

CA INDEXING COPYRIGHT (C) 2003 AMERICAN CHEMICAL SOCIETY (ACS)

FILE 'USPAT2' ENTERED AT 10:17:55 ON 29 DEC 2003

CA INDEXING COPYRIGHT (C) 2003 AMERICAN CHEMICAL SOCIETY (ACS)

=> d bib abs hitrn tot 131

L31 ANSWER 1 OF 11 USPATFULL on STN

AN 2003:158955 USPATFULL

TI Long lasting synthetic glucagon-like peptide {GLP-1}

IN Bridon, Dominique P., Outremont, CANADA
L' Archeveque, Benoit, Laval, CANADA
Ezrin, Alan M., Moraga, CA, UNITED STATES
Holmes, Darren L., Montreal, CANADA
Leblanc, Anouk, Montreal, CANADA
Pierre, Serge St., Ile Bizard, CANADA

PI US 2003108568 A1 20030612

AI US 2002-288340 A1 20021104 (10)

RLI Division of Ser. No. US 2000-657332, filed on 7 Sep 2000, GRANTED, Pat.
No. US 6514500

PRAI US 1999-159783P 19991015 (60)

DT Utility

FS APPLICATION

LREP Michael R. Ward, Morrison & Foerster LLP, 425 Market Street, San Francisco, CA, 94105-2482

CLMN Number of Claims: 19

ECL Exemplary Claim: 1

DRWN No Drawings

LN.CNT 2344

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB Modified insulinotropic peptides are disclosed. The modified insulinotropic peptides are capable of forming a peptidase stabilized insulinotropic peptide. The modified insulinotropic peptides are capable of forming covalent bonds with one or more blood components to form a conjugate. The conjugates may be formed in vivo or ex vivo. The modified peptides are administered to treat humans with diabetes and other related diseases.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

IT 309729-73-5
(lasting insulinotropic pepwith antidiabetic activity)

IT 308245-55-8 308806-01-1 308815-99-8
309729-80-4
(long lasting insulinotropic peptides with antidiabetic activity)

IT 308244-92-0P 308249-19-6P 309728-25-4P
309729-78-0P 309729-82-6P

(long lasting insulintropic peptides with antidiabetic activity)

L31 ANSWER 2 OF 11 USPTAFULL on STN
 AN 2003:158954 USPTAFULL
 TI Long lasting synthetic glucagon-like peptide (GLP-1)
 IN Bridon, Dominique P., Outremont, CANADA
 L'Archeveque, Benoit, Laval, CANADA
 Ezrin, Alan M., Moraga, CA, UNITED STATES
 Holmes, Darren L., Montreal, CANADA
 Leblanc, Anouk, Montreal, CANADA
 St. Pierre, Serge, Ile Bizard, CANADA
 PI US 2003108567 A1 20030612
 AI US 2002-287892 A1 20021104 (10)
 RLI Division of Ser. No. US 2000-657332, filed on 7 Sep 2000, GRANTED, Pat.
 No. US 6514500
 PRAI US 1999-159783P 19991015 (60)
 DT Utility
 FS APPLICATION
 LREP Michael R. Ward, Morrison & Foerster LLP, 425 Market Street, San
 Francisco, CA, 94105-2482
 CLMN Number of Claims: 19
 ECL Exemplary Claim: 1
 DRWN No Drawings
 LN.CNT 2359
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.
 AB Modified insulintropic peptides are disclosed. The modified
 insulintropic peptides are capable of forming a peptidase stabilized
 insulintropic peptide. The modified insulintropic peptides are capable
 of forming covalent bonds with one or more blood components to form a
 conjugate. The conjugates may be formed in vivo or ex vivo. The modified
 peptides are administered to treat humans with diabetes and other
 related diseases.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

IT 309729-73-5
 (lasting insulintropic pepwith antidiabetic activity)
 IT 308245-55-8 308806-01-1 308815-99-8
 309729-80-4
 (long lasting insulintropic peptides with antidiabetic activity)
 IT 308244-92-0P 308249-19-6P 309728-25-4P
 309729-78-0P 309729-82-6P
 (long lasting insulintropic peptides with antidiabetic activity)

L31 ANSWER 3 OF 11 USPTAFULL on STN
 AN 2003:127606 USPTAFULL
 TI Exendins, exendin agonists, and methods for their use
 IN Beeley, Nigel Robert Arnold, Solana Beach, CA, UNITED STATES
 Prickett, Kathryn S., San Diego, CA, UNITED STATES
 Bhavsar, Sunil, San Diego, CA, UNITED STATES
 PI US 2003087821 A1 20030508
 AI US 2002-187051 A1 20020628 (10)
 RLI Continuation of Ser. No. US 1998-3869, filed on 7 Jan 1998, PENDING
 PRAI US 1997-34905P 19970107 (60)
 US 1997-55404P 19970808 (60)
 US 1997-66029P 19971114 (60)
 US 1997-65442P 19971114 (60)
 DT Utility
 FS APPLICATION
 LREP Lisa M. McGeehan, Brobeck, Phleger & Harrison LLP, 12390 El Camino Real,
 San Diego, CA, 92130-2081
 CLMN Number of Claims: 31
 ECL Exemplary Claim: 1
 DRWN 10 Drawing Page(s)

LN.CNT 3914

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB Methods for treating conditions or disorders which can be alleviated by reducing food intake are disclosed which comprise administration of an effective amount of an exendin or an exendin agonist, alone or in conjunction with other compounds or compositions that affect satiety. The methods are useful for treating conditions or disorders, including obesity, Type II diabetes, eating disorders, and insulin-resistance syndrome. The methods are also useful for lowering the plasma glucose level, lowering the plasma lipid level, reducing the cardiac risk, reducing the appetite, and reducing the weight of subjects. Pharmaceutical compositions for use in the methods of the invention are also disclosed.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

IT 158345-16-5P 203743-29-7P 203743-31-1P
203743-32-2P 203743-33-3P 203743-35-5P
203743-36-6P 203743-37-7P 203743-38-8P
203743-39-9P 203743-41-3P 203743-45-7P
203743-46-8P 203743-47-9P 203743-53-7P
203743-54-8P 210829-41-7P 210829-46-2P
210830-02-7P 210830-13-0P 210830-31-2P
210830-35-6P 210830-59-4P
(preparation of exendin peptides for the reduction of food intake)

L31 ANSWER 4 OF 11 USPATFULL on STN

AN 2003:127605 USPATFULL

TI Novel exendin agonist formulations and methods of administration thereof

IN Young, Andrew A., La Jolla, CA, UNITED STATES

Kolterman, Orville G., Poway, CA, UNITED STATES

PI US 2003087820 A1 20030508

AI US 2002-157224 A1 20020528 (10)

RLI Continuation-in-part of Ser. No. US 2001-889330, filed on 27 Dec 2001,
PENDING A 371 of International Ser. No. WO 2000-US902, filed on 14 Jan
2000, PENDING

PRAI US 1999-116380P 19990114 (60)

US 2000-175365P 20000110 (60)

DT Utility

FS APPLICATION

LREP Molly A. Holman, Ph.D., Amylin Pharmaceuticals, Inc., 9373 Towne Centre
Drive, San Diego, CA, 92121

CLMN Number of Claims: 40

ECL Exemplary Claim: 1

DRWN 25 Drawing Page(s)

LN.CNT 3512

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB Novel exendin and exendin agonist compound formulations and dosages and methods of administration thereof are provided. These compositions and methods are useful in treating diabetes and conditions that would be benefited by lowering plasma glucose or delaying and/or slowing gastric emptying or inhibiting food intake.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

IT 522007-08-5 522007-09-6 522007-10-9
522007-12-1 522007-13-2 522007-15-4
522007-16-5 522007-17-6 522007-18-7
522007-24-5 522007-25-6 522007-28-9
522007-29-0 522007-30-3 522007-31-4
522007-32-5

(unclaimed protein sequence; novel exendin agonist formulations and
methods of administration thereof)

L31 ANSWER 5 OF 11 USPATFULL on STN

AN 2003:51546 USPATFULL
TI Use of exendins and agonists thereof for modulation of triglyceride levels and treatment of dyslipidemia
IN Kolterman, Orville G., Poway, CA, UNITED STATES
Young, Andrew A., Point Loma, CA, UNITED STATES
PA Amylin Pharmaceuticals, Inc. (U.S. corporation)
PI US 2003036504 A1 20030220
AI US 2001-756690 A1 20010109 (9)
PRAI US 2000-175365P 20000110 (60)
DT Utility
FS APPLICATION
LREP BROBECK, PHLEGER & HARRISON LLP, 12390 EL CAMINO REAL, SAN DIEGO, CA, 92130
CLMN Number of Claims: 40
ECL Exemplary Claim: 1
DRWN 5 Drawing Page(s)
LN.CNT 5350
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Methods for modulating the levels of plasma triglyceride and other lipids in a subject which comprise administration of an effective amount of an exendin or an exendin agonist, alone or in conjunction with other compounds or compositions that lower blood triglyceride and/or other lipid levels.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

IT 284676-24-0

(unclaimed protein sequence; methods using an exendin or related substance for glucagon suppression)

L31 ANSWER 6 OF 11 USPATFULL on STN

AN 2003:33172 USPATFULL
TI Long lasting synthetic glucagon like peptide {GLP-!}
IN Bridon, Dominique P., Outremont, CANADA
L'Archeveque, Benoit, Laval, CANADA
Ezrin, Alan M., Moraga, CA, United States
Holmes, Darren L., Montreal, CANADA
Leblanc, Anouk, Montreal, CANADA
St. Pierre, Serge, Ile Bizard, CANADA
PA Conjuchem, Inc., Montreal, CANADA (non-U.S. corporation)
PI US 6514500 B1 20030204
AI US 2000-657332 20000907 (9)
PRAI US 1999-159783P 19991015 (60)
DT Utility
FS GRANTED
EXNAM Primary Examiner: Housel, James; Assistant Examiner: Lucas, Zachariah
LREP Morrison & Foerster LLP
CLMN Number of Claims: 2
ECL Exemplary Claim: 1
DRWN 0 Drawing Figure(s); 0 Drawing Page(s)
LN.CNT 2251
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Modified insulinotropic peptides are disclosed. The modified insulinotropic peptides are capable of forming a peptidase stabilized insulinotropic peptide. The modified insulinotropic peptides are capable of forming covalent bonds with one or more blood components to form a conjugate. The conjugates may be formed in vivo or ex vivo. The modified peptides are administered to treat humans with diabetes and other related diseases.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

IT 309729-73-5

(lasting insulinotropic pepwith antidiabetic activity)

IT 308245-55-8 308806-01-1 308815-99-8

309729-80-4

(long lasting insulinitropic peptides with antidiabetic activity)

IT 308244-92-0P 308249-19-6P 309728-25-4P

309729-78-0P 309729-82-6P

(long lasting insulinitropic peptides with antidiabetic activity)

L31 ANSWER 7 OF 11 USPTATFLL on STN

AN 2003:13287 USPTATFLL

TI Use of exendins and agonists thereof for the treatment of gestational diabetes mellitus

IN Hiles, Richard A., San Diego, CA, United States

Prickett, Kathryn S., San Diego, CA, United States

PA Amylin Pharmaceuticals, Inc., San Diego, CA, United States (U.S. corporation)

PI US 6506724 B1 20030114

AI US 1999-323867 19990601 (9)

DT Utility

FS GRANTED

EXNAM Primary Examiner: Celsa, Bennett

LREP Brobeck, Phleger & Harrison LLP

CLMN Number of Claims: 13

ECL Exemplary Claim: 1

DRWN 3 Drawing Figure(s); 4 Drawing Page(s)

LN.CNT 5263

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB Methods for treating gestational diabetes which comprise administration of an effective amount of an exendin or an exendin agonist, alone or in conjunction with other compounds or compositions that lower blood glucose levels.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

IT 158345-16-5P 203743-29-7P 203743-31-1P

203743-32-2P 203743-33-3P 203743-35-5P

203743-36-6P 203743-37-7P 203743-38-8P

203743-41-3P 203743-45-7P 203743-46-8P

203743-47-9P 210830-02-7P 210830-13-0P

210830-35-6P 210830-59-4P 284676-24-0P

312932-20-0P 312932-28-8P 312933-83-8P

312949-21-6P 312949-26-1P

(use of exendins and agonists thereof for treatment of gestational diabetes mellitus in relation to combination with insulin or amylin agonist)

L31 ANSWER 8 OF 11 USPTATFLL on STN

AN 2002:251713 USPTATFLL

TI USE OF EXENDINS AND AGONISTS THEREOF FOR THE REDUCTION OF FOOD INTAKE

IN BEELEY, NIGEL ROBERT ARNOLD, SOLANA BEACH, CA, UNITED STATES

PRICKETT, KATHRYN S., SAN DIEGO, CA, UNITED STATES

BHAVSAR, SUNIL, SAN DIEGO, CA, UNITED STATES

PI US 2002137666 A1 20020926

AI US 1998-3869 A1 19980107 (9)

PRAI US 1997-34905P 19970107 (60)

US 1997-55404P 19970808 (60)

US 1997-66029P 19971114 (60)

US 1997-65442P 19971114 (60)

DT Utility

FS APPLICATION

LREP LYON & LYON LLP, 633 WEST FIFTH STREET, SUITE 4700, LOS ANGELES, CA, 90071

CLMN Number of Claims: 31

ECL Exemplary Claim: 1

DRWN 11 Drawing Page(s)

LN.CNT 3909

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB Methods for treating conditions or disorders which can be alleviated by reducing food intake are disclosed which comprise administration of an effective amount of an exendin or an exendin agonist, alone or in conjunction with other compounds or compositions that affect satiety. The methods are useful for treating conditions or disorders, including obesity, Type II diabetes, eating disorders, and insulin-resistance syndrome. The methods are also useful for lowering the plasma glucose level, lowering the plasma lipid level, reducing the cardiac risk, reducing the appetite, and reducing the weight of subjects. Pharmaceutical compositions for use in the methods of the invention are also disclosed.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

IT 158345-16-5P 203743-29-7P 203743-31-1P
203743-32-2P 203743-33-3P 203743-35-5P
203743-36-6P 203743-37-7P 203743-38-8P
203743-39-9P 203743-41-3P 203743-45-7P
203743-46-8P 203743-47-9P 203743-53-7P
203743-54-8P 210829-41-7P 210829-46-2P
210830-02-7P 210830-13-0P 210830-31-2P
210830-35-6P 210830-59-4P
(preparation of exendin peptides for the reduction of food intake)

L31 ANSWER 9 OF 11 USPATFULL on STN

AN 2002:92629 USPATFULL

TI Long lasting insulinotropic peptides

IN Bridon, Dominique P., Outremont, CANADA

L'Archeveque, Benoit, Leval, CANADA

Ezrin, Alan M., Moraga, CA, UNITED STATES

Holmes, Darreñ L., Montreal, CANADA

Leblanc, Anouk, Montreal, CANADA

St. Pierre, Serge, Ile Bizard, CANADA

PI US 2002049153 A1 20020425

US 6593295 B2 20030715

AI US 2001-876388 A1 20010606 (9)

RLI Division of Ser. No. US 2000-623618, filed on 5 Sep 2000, PENDING A 371
of International Ser. No. WO 2000-US13563, filed on 17 May 2000, UNKNOWN

PRAI US 1999-159783P 19991015 (60)

US 1999-134406P 19990517 (60)

DT Utility

FS APPLICATION

LREP Michael R. Ward, Morrison & Foerster LLP, 425 Market Street, San
Francisco, CA, 94105-2482

CLMN Number of Claims: 19

ECL Exemplary Claim: 1

DRWN No Drawings

LN.CNT 2355

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB Modified insulinotropic peptides are disclosed. The modified insulinotropic peptides are capable of forming a peptidase stabilized insulinotropic peptide. The modified insulinotropic peptides are capable of forming covalent bonds with one or more blood components to form a conjugate. The conjugates may be formed in vivo or ex vivo. The modified peptides are administered to treat humans with diabetes and other related diseases.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

IT 309729-73-5
(lasting insulinotropic pepwith antidiabetic activity)

IT 308245-55-8 308806-01-1 308815-99-8
309729-80-4

(long lasting insulinotropic peptides with antidiabetic activity)

IT 308244-92-0P 308249-19-6P 309728-25-4P
 309729-78-0P 309729-82-6P
 (long lasting insulintropic peptides with antidiabetic activity)

L31 ANSWER 10 OF 11 USPATFULL on STN
 AN 2001:226593 USPATFULL
 TI Long lasting insulintropic peptides
 IN Bridon, Dominique P., Outremont, Canada
 L'Archeveque, Benoit, Laval, Canada
 Ezrin, Alan M., Moraga, CA, United States
 Holmes, Darren L., Montreal, Canada
 Leblanc, Anouk, Montreal, Canada
 St. Pierre, Serge, Ile Bizard, Canada
 PA Conjuchem, Inc., Montreal, Canada (non-U.S. corporation)
 PI US 6329336 B1 20011211
 WO 2000069911 20001123
 AI US 2000-623618 20000905 (9)
 WO 2000-US13563 20000517
 20000905 PCT 371 date
 20000905 PCT 102(e) date
 PRAI US 1999-134406P 19990517 (60)
 US 1999-159783P 19991015 (60)
 DT Utility
 FS GRANTED
 EXNAM Primary Examiner: Horlick, Kenneth R.; Assistant Examiner: Strzelecka, Teresa
 LREP Morrison & Foerster LLP
 CLMN Number of Claims: 14
 ECL Exemplary Claim: 1
 DRWN No Drawings
 LN.CNT 2101

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB Modified insulintropic peptides are disclosed. The modified insulintropic peptides are capable of forming a peptidase stabilized insulintropic peptide. The modified insulintropic peptides are capable of forming covalent bonds with one or more blood components to form a conjugate. The conjugates may be formed in vivo or ex vivo. The modified peptides are administered to treat humans with diabetes and other related diseases.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

IT 309729-73-5
 (lasting insulintropic pepwith antidiabetic activity)
 IT 308245-55-8 308806-01-1 308815-99-8
 309729-80-4
 (long lasting insulintropic peptides with antidiabetic activity)
 IT 308244-92-0P 308249-19-6P 309728-25-4P
 309729-78-0P 309729-82-6P
 (long lasting insulintropic peptides with antidiabetic activity)

L31 ANSWER 11 OF 11 USPAT2 on STN
 AN 2002:92629 USPAT2
 TI Long lasting insulintropic peptides
 IN Bridon, Dominique P., Outremont, CANADA
 L'Archeveque, Benoit, Laval, CANADA
 Ezrin, Alan M., Moraga, CA, United States
 Holmes, Darren L., Montreal, CANADA
 Leblanc, Anouk, Montreal, CANADA
 St. Pierre, Serge, Ile Bizard, CANADA
 PA Conjuchem, Inc., Montreal, CANADA (non-U.S. corporation)
 PI US 6593295 B2 20030715
 AI US 2001-876388 20010606 (9)
 RLI Division of Ser. No. US 623618, now patented, Pat. No. US 6329336

PRAI US 1999-134406P 19990517 (60)
US 1999-159783P 19991015 (60)
DT Utility
FS GRANTED
EXNAM Primary Examiner: Horlick, Kenneth R.; Assistant Examiner: Strzelecka, Teresa
LREP Morrison & Foerster LLP
CLMN Number of Claims: 29
ECL Exemplary Claim: 1
DRWN 0 Drawing Figure(s); 0 Drawing Page(s)
LN.CNT 2354

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB Modified insulintropic peptides are disclosed. The modified insulintropic peptides are capable of forming a peptidase stabilized insulintropic peptide. The modified insulintropic peptides are capable of forming covalent bonds with one or more blood components to form a conjugate. The conjugates may be formed in vivo or ex vivo. The modified peptides are administered to treat humans with diabetes and other related diseases.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

IT 309729-73-5

(lasting insulintropic peptide with antidiabetic activity)

IT 308245-55-8 308806-01-1 308815-99-8
309729-80-4

(long lasting insulintropic peptides with antidiabetic activity)

IT 308244-92-0P 308249-19-6P 309728-25-4P
309729-78-0P 309729-82-6P

(long lasting insulintropic peptides with antidiabetic activity)

=>

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OM protein - protein search, using sw model

Run on: December 23, 2003, 10:02:47 ; Search time 25 Seconds

(without alignments)
298,814 Million cell updates/sec

Title: US-09-889-331a-47

Perfect score: 121
Sequence: 1 XXXGTXXXXXXKQXEENRLLXXXXXKNGXSGAXXXXX 40

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 696363 seqs, 186758610 residues

Total number of hits satisfying chosen parameters: 696363

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database: Published Applications AA*

1: /cgn2_6/ptodata/1/pubppa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubppa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubppa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubppa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubppa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubppa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubppa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubppa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubppa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubppa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubppa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubppa/US09C_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubppa/US10_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubppa/US10C_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubppa/US10C_NEW_PUB.pep.*
16: /cgn2_6/ptodata/1/pubppa/US60_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubppa/US60_PUBCOMB.pep.*
18: /cgn2_6/ptodata/1/pubppa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	93	76.9	36	US-09-003-869-171	Sequence 171, App
2	93	76.9	36	US-09-756-690A-171	Sequence 171, App
3	93	76.9	36	US-10-157-224A-171	Sequence 171, App
4	93	76.9	36	US-10-187-051-171	Sequence 171, App
5	93	76.9	37	US-09-003-869-99	Sequence 99, App
6	93	76.9	37	US-09-003-869-183	Sequence 183, App
7	93	76.9	37	US-09-756-690A-99	Sequence 99, App
8	93	76.9	37	US-09-756-690A-183	Sequence 183, App
9	93	76.9	37	US-10-157-224A-99	Sequence 99, App
10	93	76.9	37	US-10-157-224A-183	Sequence 183, App
11	93	76.9	37	US-10-187-051-99	Sequence 99, App
12	93	76.9	37	US-10-187-051-183	Sequence 183, App
13	93	76.9	39	US-09-003-869-35	Sequence 35, App
14	93	76.9	39	US-09-003-869-36	Sequence 36, App
15	93	76.9	39	US-09-003-869-39	Sequence 39, App

16	93	76.9	39	US-09-756-690A-35	Sequence 35, App
17	93	76.9	39	US-09-756-690A-36	Sequence 36, App
18	93	76.9	39	US-09-756-690A-39	Sequence 39, App
19	93	76.9	39	US-10-157-224A-35	Sequence 35, App
20	93	76.9	39	US-10-157-224A-36	Sequence 36, App
21	93	76.9	39	US-10-157-224A-39	Sequence 39, App
22	93	76.9	39	US-10-187-051-35	Sequence 35, App
23	93	76.9	39	US-10-187-051-36	Sequence 36, App
24	93	76.9	39	US-10-187-051-39	Sequence 39, App
25	92	76.0	35	US-09-003-869-69	Sequence 69, App
26	92	76.0	35	US-09-003-869-173	Sequence 173, App
27	92	76.0	35	US-09-756-690A-173	Sequence 173, App
28	92	76.0	35	US-10-157-224A-69	Sequence 69, App
29	92	76.0	35	US-10-157-224A-173	Sequence 173, App
30	92	76.0	35	US-10-187-051-69	Sequence 69, App
31	92	76.0	35	US-10-187-051-173	Sequence 173, App
32	92	76.0	35	US-09-003-869-67	Sequence 67, App
33	92	76.0	35	US-09-003-869-170	Sequence 170, App
34	92	76.0	36	US-09-003-869-184	Sequence 184, App
35	92	76.0	36	US-09-756-690A-184	Sequence 184, App
36	92	76.0	36	US-10-157-224A-184	Sequence 184, App
37	92	76.0	36	US-10-157-224A-170	Sequence 170, App
38	92	76.0	36	US-10-157-224A-184	Sequence 184, App
39	92	76.0	36	US-09-756-690A-184	Sequence 184, App
40	92	76.0	36	US-10-157-224A-184	Sequence 184, App
41	92	76.0	36	US-10-157-224A-170	Sequence 170, App
42	92	76.0	36	US-10-157-224A-184	Sequence 184, App
43	92	76.0	36	US-10-187-051-67	Sequence 67, App
44	92	76.0	36	US-10-187-051-170	Sequence 170, App
45	92	76.0	36	US-10-187-051-184	Sequence 184, App
46	92	76.0	36	US-09-003-869-65	Sequence 65, App
47	92	76.0	37	US-09-003-869-83	Sequence 83, App
48	92	76.0	37		
49	92	76.0	37		
50	92	76.0	37		

ALIGNMENTS

RESULT 1
US-09-003-869-171
Sequence 171, Application US/09003869A
Patent No. US20020137666A1
GENERAL INFORMATION:
APPLICANT: BEELEY, NIGEL ROBERT ARNOLD
APPLICANT: BEELEY, NIGEL ROBERT ARNOLD
APPLICANT: BEELEY, NIGEL ROBERT ARNOLD
TITLE OF INVENTION: USE OF EXTENDING AND AGONISTS THEREOF FOR
FILE REFERENCE: 231/181
CURRENT APPLICATION NUMBER: US/09/003,869A
CURRENT FILING DATE: 1998-01-07
EARLIER APPLICATION NUMBER: US 60/034,905
EARLIER FILING DATE: 1997-01-07
EARLIER APPLICATION NUMBER: US 60/055,404
EARLIER FILING DATE: 1997-08-08
EARLIER APPLICATION NUMBER: US 60/065,442
EARLIER FILING DATE: 1997-11-14
EARLIER APPLICATION NUMBER: US 60/066,029
EARLIER FILING DATE: 1997-11-14
NUMBER OF SEQ. ID NOS: 188
SOFTWARE: fastseq for Windows Version 3.0
SEQ ID NO 171
LENGTH: 36
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: artificially synthesized sequence of novel extendin agonist
NAME/KEY: AMIDATION
LOCATION: (36)...(36)

OTHER INFORMATION: amidated Pro (Prolinamide)
US-09-003-869-171

Query Match
Best Local Similarity 76.9%; Score 93; DB 10; Length 36;
Matches 21; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 4 GTXXXXXSKQEEAVRLXXXXLKNKGXSSGA 35
DB 4 GTFTSDASKQLEBEAVRLFIEFLKNGGPPSSGA 35

RESULT 2
US-09-756-690A-171
Sequence 171, Application US/09756690A
Publication No. US20030036504A1
GENERAL INFORMATION:
APPLICANT: KOLTERMAN, ORVILLE G.
APPLICANT: YOUNG, ANDREW A.
TITLE OF INVENTION: USE OF EXTENDING AND AGONISTS THEREOF FOR MODULATION OF
FILE REFERENCE: 249/124
CURRENT APPLICATION NUMBER: US/09/756,690A
CURRENT FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/175,365
PRIOR FILING DATE: 2000-01-10
NUMBER OF SEQ ID NOS: 188
SOFTWARE: PatentIn Ver 2.1
SEQ ID NO 171
LENGTH: 36
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE: Description of Artificial Sequence: Exendin Agonist
FEATURE:
OTHER INFORMATION: c-term amidation
US-09-756-690A-171

Query Match
Best Local Similarity 76.9%; Score 93; DB 11; Length 36;
Matches 21; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 4 GTXXXXXSKQEEAVRLXXXXLKNKGXSSGA 35
DB 4 GTFTSDASKQLEBEAVRLFIEFLKNGGPPSSGA 35

RESULT 3
US-10-157-224A-171
Sequence 171, Application US/10157224A
Publication No. US20030087820A1
GENERAL INFORMATION:
APPLICANT: KOLTERMAN, ORVILLE G.
APPLICANT: YOUNG, ANDREW A.
TITLE OF INVENTION: NOVEL EXENDIN AGONIST FORMULATIONS AND METHODS OF
FILE REFERENCE: 02001-050
CURRENT APPLICATION NUMBER: US/10/157,224A
CURRENT FILING DATE: 2002-05-28
PRIOR APPLICATION NUMBER: 09/889,330
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: PCT/US00/00902
PRIOR FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: 60/116,380
PRIOR FILING DATE: 1999-01-14
PRIOR APPLICATION NUMBER: 60/175,365
PRIOR FILING DATE: 2000-01-10
NUMBER OF SEQ ID NOS: 188
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 171
LENGTH: 36
TYPE: PRT
ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Exendin Agonist
FEATURE:
OTHER INFORMATION: c-term amidation
US-10-157-224A-171

Query Match
Best Local Similarity 76.9%; Score 93; DB 15; Length 36;
Matches 21; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 4 GTXXXXXSKQEEAVRLXXXXLKNKGXSSGA 35
DB 4 GTFTSDASKQLEBEAVRLFIEFLKNGGPPSSGA 35

RESULT 4
US-10-187-051-171
Sequence 171, Application US/10187051
Publication No. US20030087821A1
GENERAL INFORMATION:
APPLICANT: BEBELEY, NIGEL ROBERT ARNOLD
APPLICANT: PRICKETT, KATHRYN S.
APPLICANT: BHAVSAR, SUNIL
TITLE OF INVENTION: USE OF EXTENDING AND AGONISTS THEREOF FOR
FILE REFERENCE: 231/181
CURRENT APPLICATION NUMBER: US/10/187,051
CURRENT FILING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: US/09/003,869
PRIOR FILING DATE: 1998-01-07
PRIOR APPLICATION NUMBER: US 60/034,905
PRIOR FILING DATE: 1997-01-07
PRIOR APPLICATION NUMBER: US 60/055,404
PRIOR FILING DATE: 1997-08-08
PRIOR APPLICATION NUMBER: US 60/065,442
PRIOR FILING DATE: 1997-11-14
PRIOR APPLICATION NUMBER: US 60/066,029
PRIOR FILING DATE: 1997-11-14
NUMBER OF SEQ ID NOS: 188
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 171
LENGTH: 36
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: artificially synthesized sequence of novel exendin
OTHER INFORMATION: agonist
OTHER INFORMATION: compound
FEATURE:
NAME/KEY: AMIDATION
LOCATION: (36)...(36)
OTHER INFORMATION: amidated Pro (Prolinamide)
US-10-187-051-171

Query Match
Best Local Similarity 76.9%; Score 93; DB 15; Length 36;
Matches 21; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 4 GTXXXXXSKQEEAVRLXXXXLKNKGXSSGA 35
DB 4 GTFTSDASKQLEBEAVRLFIEFLKNGGPPSSGA 35

RESULT 5
US-09-003-869-99
Sequence 99, Application US/09003869A
Patent No. US2002013766A1
GENERAL INFORMATION:
APPLICANT: BEBELEY, NIGEL ROBERT ARNOLD
APPLICANT: PRICKETT, KATHRYN S.
APPLICANT: BHAVSAR, SUNIL
TITLE OF INVENTION: USE OF EXTENDING AND AGONISTS THEREOF FOR
FILE REFERENCE: THE REDUCTION OF FOOD INTAKE

FILE REFERENCE: 231/181
CURRENT APPLICATION NUMBER: US/09/003,869A
CURRENT FILING DATE: 1998-01-07
EARLIER APPLICATION NUMBER: US 60/034,905
EARLIER FILING DATE: 1997-01-07
EARLIER APPLICATION NUMBER: US 60/055,404
EARLIER FILING DATE: 1997-08-08
EARLIER APPLICATION NUMBER: US 60/065,442
EARLIER FILING DATE: 1997-11-14
EARLIER APPLICATION NUMBER: US 60/066,029
EARLIER FILING DATE: 1997-11-14
NUMBER OF SEQ ID NOS: 188
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 99
LENGTH: 37
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: artificially synthesized sequence of novel extendin agonist
OTHER INFORMATION: compound
FEATURE:
OTHER INFORMATION: Xaa in positions 31, 36 and 37 stands for homoproline.
FEATURE:
NAME/KEY: AMIDATION
LOCATION: (37)...(37)
OTHER INFORMATION: amidated hPro (homoprolinamide)
US-09-003-869-99
Query Match 76.9%; Score 93; DB 10; Length 37;
Best Local Similarity 68.8%; Pred. No. 2,1e-09;
Matches 22; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 4 GTXXXXXSKQEEBAVRLXXXXLKNKGXSSGA 35
DB 4 GTFTSDASKQMEBAVRLFIWLKNGXSSGA 35
RESULT 6
US-09-003-869-183
Sequence 183, Application US/09003869A
Patent No. US2002013766A1
GENERAL INFORMATION:
APPLICANT: BEELEY, NIGEL ROBERT ARNOLD
APPLICANT: PRICKETT, KATHRYN S.
APPLICANT: BHAVSAR, SUNIL
TITLE OF INVENTION: USE OF EXTENDIN AND AGONISTS THEREOF FOR
TITLE OF INVENTION: THE REDUCTION OF FOOD INTAKE
FILE REFERENCE: 231/181
CURRENT APPLICATION NUMBER: US/09/003,869A
CURRENT FILING DATE: 1998-01-07
EARLIER APPLICATION NUMBER: US 60/034,905
EARLIER FILING DATE: 1997-01-07
EARLIER APPLICATION NUMBER: US 60/055,404
EARLIER FILING DATE: 1997-08-08
EARLIER APPLICATION NUMBER: US 60/065,442
EARLIER FILING DATE: 1997-11-14
EARLIER APPLICATION NUMBER: US 60/066,029
EARLIER FILING DATE: 1997-11-14
NUMBER OF SEQ ID NOS: 188
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 183
LENGTH: 37
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: artificially synthesized sequence of novel extendin agonist
OTHER INFORMATION: compound
FEATURE:
OTHER INFORMATION: Xaa in positions 31, 36 and 37 stands for n-methylalanine.
FEATURE:
NAME/KEY: AMIDATION
LOCATION: (37)...(37)
OTHER INFORMATION: amidated Nmeala (n-methylalaninamide)

US-09-003-869-183
Query Match 76.9%; Score 93; DB 10; Length 37;
Best Local Similarity 68.8%; Pred. No. 2,1e-09;
Matches 22; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 4 GTXXXXXSKQEEBAVRLXXXXLKNKGXSSGA 35
DB 4 GTFTSDASKQMEBAVRLFIWLKNGXSSGA 35
RESULT 7
US-09-756-690A-99
Sequence 99, Application US/09756690A
Publication No. US20030036504A1
GENERAL INFORMATION:
APPLICANT: KOLTERMAN, ORVILLE G.
APPLICANT: YOUNG, ANDREW A.
TITLE OF INVENTION: USE OF EXTENDIN AND AGONISTS THEREOF FOR MODULATION OF
TITLE OF INVENTION: TRIGLYCERIDE LEVELS AND TREATMENT OF DYSLIPIDEMIA
FILE REFERENCE: 249/124
CURRENT APPLICATION NUMBER: US/09/756,690A
CURRENT FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/175,365
PRIOR FILING DATE: 2000-01-10
NUMBER OF SEQ ID NOS: 188
SOFTWARE: PatentIn Ver 2.1
SEQ ID NO 99
LENGTH: 37
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Extendin Agonist
FEATURE:
NAME/KEY: MOD RES
LOCATION: (31)
OTHER INFORMATION: hPro
FEATURE:
NAME/KEY: MOD RES
LOCATION: (36)
OTHER INFORMATION: hPro
FEATURE:
NAME/KEY: MOD RES
LOCATION: (37)
OTHER INFORMATION: hPro
FEATURE:
OTHER INFORMATION: c-term amidation
US-09-756-690A-99
Query Match 76.9%; Score 93; DB 11; Length 37;
Best Local Similarity 68.8%; Pred. No. 2,1e-09;
Matches 22; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 4 GTXXXXXSKQEEBAVRLXXXXLKNKGXSSGA 35
DB 4 GTFTSDASKQMEBAVRLFIWLKNGXSSGA 35
RESULT 8
US-09-756-690A-183
Sequence 183, Application US/09756690A
Publication No. US20030036504A1
GENERAL INFORMATION:
APPLICANT: KOLTERMAN, ORVILLE G.
APPLICANT: YOUNG, ANDREW A.
TITLE OF INVENTION: USE OF EXTENDIN AND AGONISTS THEREOF FOR MODULATION OF
TITLE OF INVENTION: TRIGLYCERIDE LEVELS AND TREATMENT OF DYSLIPIDEMIA
FILE REFERENCE: 249/124
CURRENT APPLICATION NUMBER: US/09/756,690A
CURRENT FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/175,365
PRIOR FILING DATE: 2000-01-10
NUMBER OF SEQ ID NOS: 188

SOFTWARE: Patentlin Ver 2.1
SEQ ID NO 183
LENGTH: 37
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Exendin Agonist
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (31)
OTHER INFORMATION: NMeala
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (36)
OTHER INFORMATION: NMeala
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (37)
OTHER INFORMATION: NMeala
FEATURE:
OTHER INFORMATION: c-term amidation
US-09-756-690A-183

Query Match 76.9%; Score 93; DB 11; Length 37;
Best Local Similarity 68.8%; Pred. No. 2.1e-09;
Matches 22; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 4 GTXXXXXSKOXEEAVRLXXXXLKNKGXSSGA 35
DB 4 GTFTSLSKQMEEEAVRLFIEWLKNKGXSSGA 35

RESULT 9
US-10-157-224A-99
Sequence 99, Application US/10157224A
Publication No. US20030087820A1
GENERAL INFORMATION:
APPLICANT: YOUNG, ANDREW A.
APPLICANT: KOLTERMAN, ORVILLE G.
TITLE OF INVENTION: NOVEL EXENDIN AGONIST FORMULATIONS AND METHODS OF
FILE REFERENCE: 02001-050
CURRENT APPLICATION NUMBER: US/10/157,224A
CURRENT FILING DATE: 2002-05-28
PRIOR APPLICATION NUMBER: 09/889,330
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: PCT/US00/00902
PRIOR FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: 60/116,380
PRIOR FILING DATE: 1999-01-14
PRIOR APPLICATION NUMBER: 60/175,365
PRIOR FILING DATE: 2000-01-10
NUMBER OF SEQ ID NOS: 188
SOFTWARE: Patentlin Ver. 2.1
SEQ ID NO 99
LENGTH: 37
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Exendin Agonist
FEATURE:
OTHER INFORMATION: c-term amidation
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (31)
OTHER INFORMATION: Homoproline
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (36)
OTHER INFORMATION: Homoproline
US-10-157-224A-99

Query Match 76.9%; Score 93; DB 15; Length 37;

Best Local Similarity 68.8%; Pred. No. 2.1e-09;
Matches 22; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 4 GTXXXXXSKOXEEAVRLXXXXLKNKGXSSGA 35
DB 4 GTFTSLSKQMEEEAVRLFIEWLKNKGXSSGA 35

RESULT 10
US-10-157-224A-183
Sequence 183, Application US/10157224A
Publication No. US20030087820A1
GENERAL INFORMATION:
APPLICANT: YOUNG, ANDREW A.
APPLICANT: KOLTERMAN, ORVILLE G.
TITLE OF INVENTION: NOVEL EXENDIN AGONIST FORMULATIONS AND METHODS OF
FILE REFERENCE: 02001-050
CURRENT APPLICATION NUMBER: US/10/157,224A
CURRENT FILING DATE: 2002-05-28
PRIOR APPLICATION NUMBER: 09/889,330
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: PCT/US00/00902
PRIOR FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: 60/116,380
PRIOR FILING DATE: 1999-01-14
PRIOR APPLICATION NUMBER: 60/175,365
PRIOR FILING DATE: 2000-01-10
NUMBER OF SEQ ID NOS: 188
SOFTWARE: Patentlin Ver. 2.1
SEQ ID NO 183
LENGTH: 37
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Exendin Agonist
FEATURE:
OTHER INFORMATION: c-term amidation
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (31)
OTHER INFORMATION: N-methylalanine
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (36)
OTHER INFORMATION: N-methylalanine
US-10-157-224A-183

Query Match 76.9%; Score 93; DB 15; Length 37;
Best Local Similarity 68.8%; Pred. No. 2.1e-09;
Matches 22; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 4 GTXXXXXSKOXEEAVRLXXXXLKNKGXSSGA 35
DB 4 GTFTSLSKQMEEEAVRLFIEWLKNKGXSSGA 35

RESULT 11
US-10-187-051-99
Sequence 99, Application US/10187051
Publication No. US20030087821A1
GENERAL INFORMATION:
APPLICANT: BEELEY, NIGEL ROBERT ARNOLD
APPLICANT: PRICKETT, KATHRYN S.
APPLICANT: BHAYSAR, SUNIL
TITLE OF INVENTION: USE OF EXENDIN AND AGONISTS THEREOF FOR
FILE REFERENCE: 231/181
CURRENT APPLICATION NUMBER: US/10/187,051
CURRENT FILING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: US/09/003,869
PRIOR FILING DATE: 1998-01-07
PRIOR APPLICATION NUMBER: US 60/034,905

PRIOR FILING DATE: 1997-01-07
PRIOR APPLICATION NUMBER: US 60/055,404
PRIOR FILING DATE: 1997-08-08
PRIOR APPLICATION NUMBER: US 60/055,442
PRIOR FILING DATE: 1997-11-14
PRIOR APPLICATION NUMBER: US 60/066,029
PRIOR FILING DATE: 1997-11-14
NUMBER OF SEQ ID NOS: 188
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 99
LENGTH: 37
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: artificially synthesized sequence of novel extendin
OTHER INFORMATION: agonist
OTHER INFORMATION: compound
FEATURE:
OTHER INFORMATION: Xaa in positions 31, 36 and 37 stands for homoproline.
FEATURE:
NAME/KEY: AMIDATION
LOCATION: (37)...(37)
OTHER INFORMATION: amidated hpro (homoprolinamide)
US-10-187-051-99

Query Match
Best Local Similarity 68.8%; Score 93; DB 15; Length 37;
Best Local Similarity 68.8%; Pred. No. 2.1e-09;
Matches 22; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 4 GTXXXXXSKXEEAVRLXXXXLKNKGXSSGA 35
DB 4 GTFTSDASKOMEAEVRLFIETLKNKGXSSGA 35

RESULT 12
US-10-187-051-183
Sequence 183, Application US/10187051
GENERAL INFORMATION:
APPLICANT: BEELEY, NIGEL ROBERT ARNOLD
APPLICANT: PRICKETT, KATHRYN S.
APPLICANT: BHAVSAR, SUNIL
TITLE OF INVENTION: USE OF EXTENDINS AND AGONISTS THEREOF FOR
FILE REFERENCE: 231/181
CURRENT APPLICATION NUMBER: US/10/187,051
CURRENT FILING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: US/09/003,869
PRIOR FILING DATE: 1998-01-07
PRIOR APPLICATION NUMBER: US 60/034,905
PRIOR FILING DATE: 1997-01-07
PRIOR APPLICATION NUMBER: US 60/055,404
PRIOR FILING DATE: 1997-08-08
PRIOR APPLICATION NUMBER: US 60/065,442
PRIOR FILING DATE: 1997-11-14
PRIOR APPLICATION NUMBER: US 60/066,029
PRIOR FILING DATE: 1997-11-14
NUMBER OF SEQ ID NOS: 188
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 183
LENGTH: 37
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: artificially synthesized sequence of novel extendin
OTHER INFORMATION: agonist
OTHER INFORMATION: compound
FEATURE:
OTHER INFORMATION: Xaa in positions 31, 36 and 37 stands for n-
OTHER INFORMATION: methylaniline.
NAME/KEY: AMIDATION
LOCATION: (37)...(37)

OTHER INFORMATION: amidated Nmeala (n-methylanilineamide)
US-10-187-051-183

Query Match
Best Local Similarity 68.8%; Score 93; DB 15; Length 37;
Best Local Similarity 68.8%; Pred. No. 2.1e-09;
Matches 22; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 4 GTXXXXXSKXEEAVRLXXXXLKNKGXSSGA 35
DB 4 GTFTSDASKOMEAEVRLFIETLKNKGXSSGA 35

RESULT 13
US-09-003-869-35
Sequence 35, Application US/09003869A
Patent No. US20020137666A1
GENERAL INFORMATION:
APPLICANT: BEELEY, NIGEL ROBERT ARNOLD
APPLICANT: PRICKETT, KATHRYN S.
APPLICANT: BHAVSAR, SUNIL
TITLE OF INVENTION: USE OF EXTENDINS AND AGONISTS THEREOF FOR
FILE REFERENCE: 231/181
CURRENT APPLICATION NUMBER: US/09/003,869A
CURRENT FILING DATE: 1998-01-07
PRIOR APPLICATION NUMBER: US 60/034,905
PRIOR FILING DATE: 1997-01-07
PRIOR APPLICATION NUMBER: US 60/055,404
PRIOR FILING DATE: 1997-08-08
PRIOR APPLICATION NUMBER: US 60/065,442
PRIOR FILING DATE: 1997-11-14
PRIOR APPLICATION NUMBER: US 60/066,029
PRIOR FILING DATE: 1997-11-14
NUMBER OF SEQ ID NOS: 188
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 35
LENGTH: 39
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: artificially synthesized sequence of novel extendin agonist
OTHER INFORMATION: compound
FEATURE:
OTHER INFORMATION: Xaa in positions 31, 36, 37 and 38 stands for thioproline.
NAME/KEY: AMIDATION
LOCATION: (39)...(39)
OTHER INFORMATION: amidated Ser (Serinamide)
US-09-003-869-35

Query Match
Best Local Similarity 76.9%; Score 93; DB 10; Length 39;
Best Local Similarity 68.8%; Pred. No. 2.2e-09;
Matches 22; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 4 GTXXXXXSKXEEAVRLXXXXLKNKGXSSGA 35
DB 4 GTFTSDASKOMEAEVRLFIETLKNKGXSSGA 35

RESULT 14
US-09-003-869-36
Sequence 36, Application US/09003869A
Patent No. US20020137666A1
GENERAL INFORMATION:
APPLICANT: BEELEY, NIGEL ROBERT ARNOLD
APPLICANT: PRICKETT, KATHRYN S.
APPLICANT: BHAVSAR, SUNIL
TITLE OF INVENTION: USE OF EXTENDINS AND AGONISTS THEREOF FOR
FILE REFERENCE: 231/181
CURRENT APPLICATION NUMBER: US/09/003,869A
CURRENT FILING DATE: 1998-01-07
PRIOR APPLICATION NUMBER: US 60/034,905
PRIOR FILING DATE: 1998-01-07

EARLIER FILING DATE: 1997-01-07
EARLIER APPLICATION NUMBER: US 60/055,404
EARLIER FILING DATE: 1997-08-08
EARLIER APPLICATION NUMBER: US 60/065,442
EARLIER FILING DATE: 1997-11-14
EARLIER APPLICATION NUMBER: US 60/066,029
EARLIER FILING DATE: 1997-11-14
NUMBER OF SEQ ID NOS: 188
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 36
LENGTH: 39
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: artificially synthesized sequence of novel extendin agonist
OTHER INFORMATION: compound
FEATURE:
OTHER INFORMATION: Xaa in positions 31, 36, 37 and 38 stands for homoproline.
FEATURE:
NAME/KEY: AMIDATION
LOCATION: (39)...(39)
OTHER INFORMATION: amidated Ser (Serinamide)
US-09-003-869-36

Query Match 76.9%; Score 93; DB 10; Length 39;
Best Local Similarity 68.8%; Pred. No. 2.2e-09;
Matches 22; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 4 GTXXXXXSKXEEAVRLXXXXLKNGXSSGA 35
DB 4 GTFTSDLSKQLEBEAVRLFIEFLKNGXSSGA 35

RESULT 15
US-09-003-869-39
Sequence 39, Application US/09003869A
Patent No. US2002013766A1
GENERAL INFORMATION:
APPLICANT: BEELEY, NIGEL ROBERT ARNOLD
APPLICANT: PRICKETT, KATHRYN S.
APPLICANT: BHAVSAR, SUNIL
TITLE OF INVENTION: USE OF EXTENDING AND AGONISTS THEREOF FOR
FILE REFERENCE: 231/181
CURRENT APPLICATION NUMBER: US/09/003,869A
EARLIER FILING DATE: 1998-01-07
EARLIER APPLICATION NUMBER: US 60/034,905
EARLIER FILING DATE: 1997-01-07
EARLIER APPLICATION NUMBER: US 60/055,404
EARLIER FILING DATE: 1997-08-08
EARLIER APPLICATION NUMBER: US 60/065,442
EARLIER FILING DATE: 1997-11-14
EARLIER APPLICATION NUMBER: US 60/066,029
EARLIER FILING DATE: 1997-11-14
NUMBER OF SEQ ID NOS: 188
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 39
LENGTH: 39
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: artificially synthesized sequence of novel extendin agonist
OTHER INFORMATION: compound
FEATURE:
OTHER INFORMATION: Xaa in positions 31, 36, 37 and 38 stands for n-methylalanine.
NAME/KEY: AMIDATION
LOCATION: (39)...(39)
OTHER INFORMATION: amidated Ser (Serinamide)
US-09-003-869-39

Query Match 76.9%; Score 93; DB 10; Length 39;
Best Local Similarity 68.8%; Pred. No. 2.2e-09;

Matches 22; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 4 GTXXXXXSKXEEAVRLXXXXLKNGXSSGA 35
DB 4 GTFTSDLSKQLEBEAVRLFIEFLKNGXSSGA 35

RESULT 16
US-09-756-690A-35
Sequence 35, Application US/09756690A
Publication No. US20030036504A1
GENERAL INFORMATION:
APPLICANT: KOLTERMAN, ORVILLE G.
APPLICANT: YOUNG, ANDREW A.
TITLE OF INVENTION: USE OF EXTENDING AND AGONISTS THEREOF FOR MODULATION OF
TRIGLYCERIDE LEVELS AND TREATMENT OF DYSLIPIDEMIA
FILE REFERENCE: 249/124
CURRENT APPLICATION NUMBER: US/09/756,690A
CURRENT FILING DATE: 2002-04-19
PRIOR FILING DATE: 2000-01-10
NUMBER OF SEQ ID NOS: 188
SOFTWARE: PatentIn Ver 2.1
SEQ ID NO: 35
LENGTH: 39
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE: Description of Artificial Sequence: Extendin Agonist
OTHER INFORMATION:
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (31)
OTHER INFORMATION: tPro
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (37)
OTHER INFORMATION: tPro
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (38)
OTHER INFORMATION: tPro
FEATURE:
OTHER INFORMATION: c-term amidation
US-09-756-690A-35

Query Match 76.9%; Score 93; DB 11; Length 39;
Best Local Similarity 68.8%; Pred. No. 2.2e-09;
Matches 22; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 4 GTXXXXXSKXEEAVRLXXXXLKNGXSSGA 35
DB 4 GTFTSDLSKQLEBEAVRLFIEFLKNGXSSGA 35

RESULT 17
US-09-756-690A-36
Sequence 36, Application US/09756690A
Publication No. US20030036504A1
GENERAL INFORMATION:
APPLICANT: KOLTERMAN, ORVILLE G.
APPLICANT: YOUNG, ANDREW A.
TITLE OF INVENTION: USE OF EXTENDING AND AGONISTS THEREOF FOR MODULATION OF
TRIGLYCERIDE LEVELS AND TREATMENT OF DYSLIPIDEMIA
FILE REFERENCE: 249/124
CURRENT APPLICATION NUMBER: US/09/756,690A
CURRENT FILING DATE: 2002-04-19
PRIOR FILING DATE: 2000-01-10
NUMBER OF SEQ ID NOS: 188

SOFTWARE: PatentIn Ver 2.1
SEQ ID NO 35
LENGTH: 39
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Exendin Agonist
FEATURE:
NAME/KEY: MOD RES
LOCATION: (31)
OTHER INFORMATION: LPro
FEATURE:
NAME/KEY: MOD RES
LOCATION: (36)
OTHER INFORMATION: LPro
FEATURE:
NAME/KEY: MOD RES
LOCATION: (37)
OTHER INFORMATION: LPro
FEATURE:
NAME/KEY: MOD RES
LOCATION: (38)
OTHER INFORMATION: LPro
FEATURE:
OTHER INFORMATION: c-term amidation
US-09-756-690A-36
76.9%: Score 93; DB 11; Length 39;
Query Match 68.8%; Pred. No. 2.2e-09;
Best Local Similarity 68.8%; 0; Mismatches 10; Indels 0; Gaps 0;
Matches 22; Conservative

QY 4 GTXXXXXSKQXEEAVRLXXXXLKNKGXSSGA 35
DB 4 GTFTSDLSKQLEEEAVRLFIEFLNKGXSSGA 35

RESULT 18
US-09-756-690A-39
Sequence 39, Application US/09756690A
Publication No. US20030036504A1
GENERAL INFORMATION:
APPLICANT: KOLTERMAN, ORVILLE G.
APPLICANT: YOUNG, ANDREW A.
TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR MODULATION OF
TITLE OF INVENTION: TRIPALYCERIDE LEVELS AND TREATMENT OF DYSLIPIDEMIA
FILE REFERENCE: 249/124
CURRENT APPLICATION NUMBER: US/09/756,690A
CURRENT FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/175,365
PRIOR FILING DATE: 2000-01-10
NUMBER OF SEQ ID NOS: 188
SOFTWARE: PatentIn Ver 2.1
SEQ ID NO 39
LENGTH: 39
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Exendin Agonist
FEATURE:
NAME/KEY: MOD RES
LOCATION: (31)
OTHER INFORMATION: MEALa
FEATURE:
NAME/KEY: MOD RES
LOCATION: (36)
OTHER INFORMATION: MEALa
FEATURE:
NAME/KEY: MOD RES
LOCATION: (37)
OTHER INFORMATION: MEALa

OTHER INFORMATION: MEALa
FEATURE:
OTHER INFORMATION: c-term amidation
US-09-756-690A-39
76.9%: Score 93; DB 11; Length 39;
Query Match 68.8%; Pred. No. 2.2e-09;
Best Local Similarity 68.8%; 0; Mismatches 10; Indels 0; Gaps 0;
Matches 22; Conservative

QY 4 GTXXXXXSKQXEEAVRLXXXXLKNKGXSSGA 35
DB 4 GTFTSDLSKQLEEEAVRLFIEFLNKGXSSGA 35

RESULT 19
US-10-157-224A-35
Sequence 35, Application US/10157224A
Publication No. US20030087820A1
GENERAL INFORMATION:
APPLICANT: YOUNG, ANDREW A.
APPLICANT: KOLTERMAN, ORVILLE G.
TITLE OF INVENTION: NOVEL EXENDIN AGONIST FORMULATIONS AND METHODS OF
TITLE OF INVENTION: ADMINISTRATION THEREOF
FILE REFERENCE: 02001-050
CURRENT APPLICATION NUMBER: US/10/157,224A
CURRENT FILING DATE: 2002-05-28
PRIOR APPLICATION NUMBER: 09/889,330
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: PCT/US00/00902
PRIOR FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: 60/116,380
PRIOR FILING DATE: 1999-01-14
PRIOR APPLICATION NUMBER: 60/175,365
PRIOR FILING DATE: 2000-01-10
NUMBER OF SEQ ID NOS: 188
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 35
LENGTH: 39
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Exendin Agonist
FEATURE:
OTHER INFORMATION: c-term amidation
FEATURE:
NAME/KEY: MOD RES
LOCATION: (31)
OTHER INFORMATION: LPro
FEATURE:
NAME/KEY: MOD RES
LOCATION: (36)
OTHER INFORMATION: LPro
FEATURE:
NAME/KEY: MOD RES
LOCATION: (38)
OTHER INFORMATION: LPro
FEATURE:
OTHER INFORMATION: LPro

US-10-157-224A-35
76.9%: Score 93; DB 15; Length 39;
Query Match 68.8%; Pred. No. 2.2e-09;
Best Local Similarity 68.8%; 0; Mismatches 10; Indels 0; Gaps 0;
Matches 22; Conservative

QY 4 GTXXXXXSKQXEEAVRLXXXXLKNKGXSSGA 35
DB 4 GTFTSDLSKQLEEEAVRLFIEFLNKGXSSGA 35

RESULT 20
US-10-157-224A-36
Sequence 36, Application US/10157224A
Publication No. US20030087820A1
GENERAL INFORMATION:
APPLICANT: YOUNG, ANDREW A.
APPLICANT: KOLTERMAN, ORVILLE G.
TITLE OF INVENTION: NOVEL EXENDIN AGONIST FORMULATIONS AND METHODS OF
TITLE OF INVENTION: ADMINISTRATION THEREOF
FILE REFERENCE: 02001-050

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Page 8

CURRENT APPLICATION NUMBER: US/10/157,224A
CURRENT FILING DATE: 2002-05-28
PRIOR APPLICATION NUMBER: 09/889,330
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: PCT/US00/00902
PRIOR FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: 60/116,380
PRIOR FILING DATE: 1999-01-14
PRIOR APPLICATION NUMBER: 60/175,365
PRIOR FILING DATE: 2000-01-10
NUMBER OF SEQ ID NOS: 188
SOFTWARE: Patent Ver. 2.1
SEQ ID NO 36
LENGTH: 39
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE: Description of Artificial Sequence: Exendin Agonist
OTHER INFORMATION: c-term amidation
FEATURE:
FEATURE:
NAME/KEY: MOD RES
LOCATION: (31)
OTHER INFORMATION: homoproline
FEATURE:
NAME/KEY: MOD RES
LOCATION: (36)..(38)
OTHER INFORMATION: homoproline
US-10-157-224A-36

Query Match 76.9%; Score 93; DB 15; Length 39;
Best Local Similarity 68.8%; Pred. No. 2,2e-09;
Matches 22; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
4 GTXXXXXSKXEEAVRLXXXXLKNKGXSSGA 35
4 GTFTSLSKQLEEEAVRLFLEFLKNKGXSSGA 35

RESULT 21
US-10-157-224A-39
Sequence 39, Application US/10157224A
Publication No. US20030087820A1
GENERAL INFORMATION:
APPLICANT: YOUNG, ANDREW A.
APPLICANT: KOLTERMAN, ORVILLE G.
TITLE OF INVENTION: NOVEL EXENDIN AGONIST FORMULATIONS AND METHODS OF
FILE REFERENCE: 02001-050
CURRENT APPLICATION NUMBER: US/10/157,224A
CURRENT FILING DATE: 2002-05-28
PRIOR APPLICATION NUMBER: 09/889,330
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: PCT/US00/00902
PRIOR FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: 60/116,380
PRIOR FILING DATE: 1999-01-14
PRIOR APPLICATION NUMBER: 60/175,365
PRIOR FILING DATE: 2000-01-10
NUMBER OF SEQ ID NOS: 188
SOFTWARE: Patent Ver. 2.1
SEQ ID NO 39
LENGTH: 39
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE: Description of Artificial Sequence: Exendin Agonist
OTHER INFORMATION: c-term amidation
FEATURE:
OTHER INFORMATION: c-term amidation

FEATURE:
NAME/KEY: MOD RES
LOCATION: (36)..(38)
OTHER INFORMATION: N-methylalanine
US-10-157-224A-39
Query Match 76.9%; Score 93; DB 15; Length 39;
Best Local Similarity 68.8%; Pred. No. 2,2e-09;
Matches 22; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
4 GTXXXXXSKXEEAVRLXXXXLKNKGXSSGA 35
4 GTFTSLSKQLEEEAVRLFLEFLKNKGXSSGA 35

RESULT 22
US-10-187-051-35
Sequence 35, Application US/10187051
Publication No. US20030087821A1
GENERAL INFORMATION:
APPLICANT: BEBLEY, NIGEL ROBERT ARNOLD
APPLICANT: PRICKETT, KATHRYN S.
TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR
REDUCTION OF FOOD INTAKE
FILE REFERENCE: 231/181
CURRENT APPLICATION NUMBER: US/10/187,051
CURRENT FILING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: US/09/003,869
PRIOR FILING DATE: 1998-01-07
PRIOR APPLICATION NUMBER: US 60/034,905
PRIOR FILING DATE: 1997-01-07
PRIOR APPLICATION NUMBER: US 60/055,404
PRIOR FILING DATE: 1997-08-08
PRIOR APPLICATION NUMBER: US 60/065,442
PRIOR FILING DATE: 1997-11-14
PRIOR APPLICATION NUMBER: US 60/066,029
PRIOR FILING DATE: 1997-11-14
NUMBER OF SEQ ID NOS: 188
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 35
LENGTH: 39
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE: artificially synthesized sequence of novel exendin
OTHER INFORMATION: agonist
OTHER INFORMATION: compound
FEATURE:
OTHER INFORMATION: Xaa in positions 31, 36, 37 and 38 stands for
OTHER INFORMATION: thioproline.
FEATURE:
NAME/KEY: AMIDATION
LOCATION: (39)..(39)
OTHER INFORMATION: amidated Ser (Serinamide)
US-10-187-051-35

Query Match 76.9%; Score 93; DB 15; Length 39;
Best Local Similarity 68.8%; Pred. No. 2,2e-09;
Matches 22; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
4 GTXXXXXSKXEEAVRLXXXXLKNKGXSSGA 35
4 GTFTSLSKQLEEEAVRLFLEFLKNKGXSSGA 35

RESULT 23
US-10-187-051-36
Sequence 36, Application US/10187051
Publication No. US20030087821A1
GENERAL INFORMATION:
APPLICANT: BEBLEY, NIGEL ROBERT ARNOLD
APPLICANT: PRICKETT, KATHRYN S.

```

APPLICANT: BHAVSAR, SUNIL
TITLE OF INVENTION: USE OF EXTENDINS AND AGONISTS THEREOF FOR
FILE REFERENCE: 231/181
CURRENT APPLICATION NUMBER: US/00/187,051
PRIOR FILING DATE: 1997-01-07
PRIOR APPLICATION NUMBER: US 60/034,905
PRIOR FILING DATE: 1997-01-07
PRIOR APPLICATION NUMBER: US 60/055,404
PRIOR FILING DATE: 1997-08-08
PRIOR APPLICATION NUMBER: US 60/065,442
PRIOR FILING DATE: 1997-11-14
PRIOR APPLICATION NUMBER: US 60/066,029
PRIOR FILING DATE: 1997-11-14
NUMBER OF SEQ ID NOS: 188
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 36
LENGTH: 39
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE: Artificially synthesized sequence of novel extendin
OTHER INFORMATION: agonist
OTHER INFORMATION: compound
FEATURE: Xaa in positions 31, 36, 37 and 38 stands for
OTHER INFORMATION: homopolymers.
FEATURE: AMIDATION
NAME/KEY: (39)...(39)
LOCATION: (39)...(39)
OTHER INFORMATION: amidated Ser (Serinamide)
US-10-187-051-36
Query Match 76.9%; Score 93; DB 15; Length 39;
Best Local Similarity 68.8%; Pred. No. 2.2e-09;
Matches 22; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 4 GTXXXXXSKOXEEAVRLXXXXLXNGXSSGA 35
DB 4 GTFTSDLSKQLEBEAVRLFIEFLKXGXS 35

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```

FEATURE: Artificially synthesized sequence of novel extendin
OTHER INFORMATION: agonist
OTHER INFORMATION: compound
FEATURE: Xaa in positions 31, 36, 37 and 38 stands for n-
OTHER INFORMATION: methylaniline.
FEATURE: AMIDATION
NAME/KEY: (39)...(39)
LOCATION: (39)...(39)
OTHER INFORMATION: amidated Ser (Serinamide)
US-10-187-051-39
Query Match 76.9%; Score 93; DB 15; Length 39;
Best Local Similarity 68.8%; Pred. No. 2.2e-09;
Matches 22; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 4 GTXXXXXSKOXEEAVRLXXXXLXNGXSSGA 35
DB 4 GTFTSDLSKQLEBEAVRLFIEFLKXGXS 35

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RESULT 25
US-09-003-869-69
Sequence 69, Application US/09003869A
Patent No. US20020137666A1
GENERAL INFORMATION: Nigel Robert Arnold
APPLICANT: BEELEY, NIGEL ROBERT ARNOLD
APPLICANT: PRICKETT, KATHRYN S.
TITLE OF INVENTION: USE OF EXTENDINS AND AGONISTS THEREOF FOR
FILE REFERENCE: 231/181
CURRENT APPLICATION NUMBER: US/09/003,869A
CURRENT FILING DATE: 1998-01-07
PRIOR FILING DATE: 1997-01-07
PRIOR APPLICATION NUMBER: US 60/034,905
PRIOR FILING DATE: 1997-08-08
PRIOR APPLICATION NUMBER: US 60/055,404
PRIOR FILING DATE: 1997-11-14
PRIOR APPLICATION NUMBER: US 60/065,442
PRIOR FILING DATE: 1997-11-14
PRIOR APPLICATION NUMBER: US 60/066,029
PRIOR FILING DATE: 1997-11-14
NUMBER OF SEQ ID NOS: 188
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 69
LENGTH: 35
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE: Artificially synthesized sequence of novel extendin agonist
OTHER INFORMATION: compound
FEATURE: AMIDATION
NAME/KEY: (35)...(35)
LOCATION: (35)...(35)
OTHER INFORMATION: amidated Ala (Alaninamide)
US-09-003-869-69
Query Match 76.0%; Score 92; DB 10; Length 35;
Best Local Similarity 65.6%; Pred. No. 2.9e-09;
Matches 21; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
QY 4 GTXXXXXSKOXEEAVRLXXXXLXNGXSSGA 35
DB 4 GTFTSDLSKQLEBEAVRLFIEFLKXGXS 35

```

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RESULT 26
US-09-003-869-173
Sequence 173, Application US/09003869A
Patent No. US20020137666A1
GENERAL INFORMATION: Nigel Robert Arnold

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US-09-889-331a-47.rapb

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APPLICANT: PRICKETT, KATHRYN S.
APPLICANT: BHASAR, SUNIL
TITLE OF INVENTION: USE OF EXTENDING AND AGONISTS THEREOF FOR
TITLE OF INVENTION: THE REDUCTION OF FOOD INTAKE
FILE REFERENCE: 231/181
CURRENT APPLICATION NUMBER: US/09/003,869A
CURRENT FILING DATE: 1998-01-07
EARLIER APPLICATION NUMBER: US 60/034,905
EARLIER FILING DATE: 1997-01-07
EARLIER APPLICATION NUMBER: US 60/055,404
EARLIER FILING DATE: 1997-08-08
EARLIER APPLICATION NUMBER: US 60/065,442
EARLIER FILING DATE: 1997-11-14
EARLIER APPLICATION NUMBER: US 60/066,029
EARLIER FILING DATE: 1997-11-14
NUMBER OF SEQ ID NOS: 188
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 173
LENGTH: 35
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE: Description of Artificial Sequence: Extendin Agonist
OTHER INFORMATION: compound
NAME/KEY: AMIDATION
LOCATION: (35)
OTHER INFORMATION: amidated Ala (Alaninamide)
US-09-003-869-173

Query Match 76.0%; Score 92; DB 10; Length 35;
Best Local Similarity 65.6%; Pred. No. 2.9e-09;
Matches 21; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

4 GTXXXXXXSKQEEAVRLXXXXLKNKGXSSGA 35
4 GTFTSDLSKQLEEEAVRLFIETFLNKGSPSSGA 35

RESULT 27
US-09-756-690A-69
Sequence 69, Application US/09756690A
Publication No. US20030036504A1
GENERAL INFORMATION:
APPLICANT: KOTTERMAN, ORVILLE G.
APPLICANT: YOUNG, ANDREW A.
TITLE OF INVENTION: USE OF EXTENDING AND AGONISTS THEREOF FOR MODULATION OF
TITLE OF INVENTION: TRIGLYCERIDE LEVELS AND TREATMENT OF DYSLIPIDEMIA
FILE REFERENCE: 249/124
CURRENT APPLICATION NUMBER: US/09/756,690A
CURRENT FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/175,365
PRIOR FILING DATE: 2000-01-10
NUMBER OF SEQ ID NOS: 188
SOFTWARE: PatentIn Ver 2.1
SEQ ID NO: 69
LENGTH: 35
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE: Description of Artificial Sequence: Extendin Agonist
OTHER INFORMATION: compound
NAME/KEY: AMIDATION
LOCATION: (35)
OTHER INFORMATION: amidated Ala (Alaninamide)
US-09-756-690A-69

Query Match 76.0%; Score 92; DB 11; Length 35;
Best Local Similarity 65.6%; Pred. No. 2.9e-09;
Matches 21; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

4 GTXXXXXXSKQEEAVRLXXXXLKNKGXSSGA 35
4 GTFTSDLSKQLEEEAVRLFIETFLNKGSPSSGA 35

RESULT 28
US-09-756-690A-173
Sequence 173, Application US/09756690A
Publication No. US20030036504A1
GENERAL INFORMATION:
APPLICANT: KOTTERMAN, ORVILLE G.
APPLICANT: YOUNG, ANDREW A.
TITLE OF INVENTION: USE OF EXTENDING AND AGONISTS THEREOF FOR MODULATION OF
TITLE OF INVENTION: TRIGLYCERIDE LEVELS AND TREATMENT OF DYSLIPIDEMIA
FILE REFERENCE: 249/124
CURRENT APPLICATION NUMBER: US/09/756,690A
CURRENT FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/175,365
PRIOR FILING DATE: 2000-01-10
NUMBER OF SEQ ID NOS: 188
SOFTWARE: PatentIn Ver 2.1
SEQ ID NO: 173
LENGTH: 35
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE: Description of Artificial Sequence: Extendin Agonist
OTHER INFORMATION: compound
NAME/KEY: AMIDATION
LOCATION: (35)
OTHER INFORMATION: amidated Ala (Alaninamide)
US-09-756-690A-173

Query Match 76.0%; Score 92; DB 11; Length 35;
Best Local Similarity 65.6%; Pred. No. 2.9e-09;
Matches 21; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

4 GTXXXXXXSKQEEAVRLXXXXLKNKGXSSGA 35
4 GTFTSDLSKQLEEEAVRLFIETFLNKGSPSSGA 35

RESULT 29
US-10-157-224A-69
Sequence 69, Application US/10157224A
Publication No. US20030087820A1
GENERAL INFORMATION:
APPLICANT: KOTTERMAN, ORVILLE G.
APPLICANT: YOUNG, ANDREW A.
TITLE OF INVENTION: NOVEL EXTENDIN AGONIST FORMULATIONS AND METHODS OF
TITLE OF INVENTION: ADMINISTRATION THEREOF
FILE REFERENCE: 02001-050
CURRENT APPLICATION NUMBER: US/10/157,224A
CURRENT FILING DATE: 2002-05-28
PRIOR APPLICATION NUMBER: 09/889,330
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: PCT/US00/00902
PRIOR FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: 60/116,380
PRIOR FILING DATE: 1999-01-14
PRIOR APPLICATION NUMBER: 60/175,365
PRIOR FILING DATE: 2000-01-10
NUMBER OF SEQ ID NOS: 188
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 69
LENGTH: 35
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE: Description of Artificial Sequence: Extendin Agonist
OTHER INFORMATION: compound
NAME/KEY: AMIDATION
LOCATION: (35)
OTHER INFORMATION: amidated Ala (Alaninamide)
US-10-157-224A-69

Query Match 76.0%; Score 92; DB 15; Length 35;
Best Local Similarity 65.6%; Pred. No. 2.9e-09;
Matches 21; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

4 GTXXXXXXSKQEEAVRLXXXXLKNKGXSSGA 35
4 GTFTSDLSKQLEEEAVRLFIETFLNKGSPSSGA 35

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Db 4 GTFTSDLSKOLEEAVRLFIETFLKNGSPSSGA 35

RESULT 30
US-10-157-224A-173
Sequence 173, Application US/10157224A
Publication No. US20030087820A1
GENERAL INFORMATION:
APPLICANT: YOUNG, ANDREW A.
APPLICANT: KOLTERMAN, ORVILLE G.
TITLE OF INVENTION: NOVEL EXENDIN AGONIST FORMULATIONS AND METHODS OF
TITLE OF INVENTION: ADMINISTRATION THEREOF
FILE REFERENCE: 02001-050
CURRENT APPLICATION NUMBER: US/10/157,224A
CURRENT FILING DATE: 2002-05-28
PRIOR APPLICATION NUMBER: 09/889,330
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: PCT/US00/00902
PRIOR FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: 60/116,380
PRIOR FILING DATE: 1999-01-14
PRIOR APPLICATION NUMBER: 60/175,365
PRIOR FILING DATE: 2000-01-10
NUMBER OF SEQ ID NOS: 188
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO: 173
LENGTH: 35
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Exendin Agonist
FEATURE:
OTHER INFORMATION: c-term amidation
US-10-157-224A-173

Query Match 76.0%; Score 92; DB 15; Length 35;
Best Local Similarity 65.6%; Pred. No. 2,9e-09;
Matches 21; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 4 GTXXXXXSKOLEEAVRLFIETFLKNGSPSSGA 35
Db 4 GTFTSDLSKOLEEAVRLFIETFLKNGSPSSGA 35

Search completed: December 23, 2003, 10:12:01
Job time : 25.5 secs

Mon Dec 29 06:32:04 2003

us-09-889-331a-47.rag

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 23, 2003, 09:59:55, Search time 36.5 Seconds
(without alignments)
173.947 Million cell updates/sec

Title: US-09-889-331A-47
Perfect score: 121
Sequence: 1 XXXGTXXXXXXKQXEEAVRLXXXLKNGXSGAXXXXX 40

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1107863 segs, 158726573 residues
Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database: A_Geneseq_19jun03:*

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23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	94	77.7	37	20	AA17618
2	94	77.7	37	22	AAE08527
3	94	77.7	37	22	AAE08527
4	94	77.7	37	22	AAE08527
5	94	77.7	37	22	AAE08527
6	94	77.7	37	22	AAE08527
7	94	77.7	37	22	AAE08527
8	94	77.7	37	22	AAE08527
9	94	77.7	37	22	AAE08527

10	93	76.9	36	22	AAE08515	Exendin agonist pe
11	93	76.9	36	22	AAE08515	Exendin agonist pe
12	93	76.9	37	20	AAE08515	Exendin agonist pe
13	93	76.9	37	20	AAE08515	Exendin agonist pe
14	93	76.9	37	21	AAE08515	Exendin agonist pe
15	93	76.9	37	21	AAE08515	Exendin agonist pe
16	93	76.9	37	21	AAE08515	Exendin agonist pe
17	93	76.9	37	21	AAE08515	Exendin agonist pe
18	93	76.9	37	22	AAE08515	Exendin agonist pe
19	93	76.9	37	22	AAE08515	Exendin agonist pe
20	93	76.9	37	22	AAE08515	Exendin agonist pe
21	93	76.9	37	22	AAE08515	Exendin agonist pe
22	93	76.9	37	22	AAE08515	Exendin agonist pe
23	93	76.9	37	22	AAE08515	Exendin agonist pe
24	93	76.9	37	22	AAE08515	Exendin agonist pe
25	93	76.9	37	22	AAE08515	Exendin agonist pe
26	93	76.9	37	22	AAE08515	Exendin agonist pe
27	93	76.9	37	22	AAE08515	Exendin agonist pe
28	93	76.9	37	22	AAE08515	Exendin agonist pe
29	93	76.9	37	22	AAE08515	Exendin agonist pe
30	93	76.9	37	22	AAE08515	Exendin agonist pe
31	93	76.9	37	22	AAE08515	Exendin agonist pe
32	93	76.9	37	22	AAE08515	Exendin agonist pe
33	93	76.9	37	22	AAE08515	Exendin agonist pe
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36	93	76.9	37	22	AAE08515	Exendin agonist pe
37	93	76.9	37	22	AAE08515	Exendin agonist pe
38	93	76.9	37	22	AAE08515	Exendin agonist pe
39	93	76.9	37	22	AAE08515	Exendin agonist pe
40	93	76.9	37	22	AAE08515	Exendin agonist pe
41	93	76.9	37	22	AAE08515	Exendin agonist pe
42	93	76.9	37	22	AAE08515	Exendin agonist pe
43	93	76.9	37	22	AAE08515	Exendin agonist pe
44	93	76.9	37	22	AAE08515	Exendin agonist pe
45	93	76.9	37	22	AAE08515	Exendin agonist pe
46	93	76.9	37	22	AAE08515	Exendin agonist pe
47	93	76.9	37	22	AAE08515	Exendin agonist pe
48	93	76.9	37	22	AAE08515	Exendin agonist pe
49	93	76.9	37	22	AAE08515	Exendin agonist pe
50	93	76.9	37	22	AAE08515	Exendin agonist pe

ALIGNMENTS

RESULT 1	AA17618	standard; peptide; 37 AA.
ID	AA17618	
XX	AA17618	
AC	AA17618	
XX	09-AUG-1999	(first entry)
DT	09-AUG-1999	
XX	09-AUG-1999	
DE	Exendin agonist peptide #84.	
XX	Exendin; agonist; Heloderma sp.; Gila monster; venom; lizard;	
KW	diabetes mellitus type I; diabetes mellitus type II; hypoglycaemia;	
KM	hypoglycaemia; plasma glucose; gastric emptying; stomach emptying.	
OS	Synthetic.	
OS	Heloderma sp.	
PN	WO9925728-A1.	
XX	WO9925728-A1.	
PD	27-MAY-1999.	
XX	27-MAY-1999.	
PF	13-NOV-1998;	98WO-US24273.
XX	13-NOV-1998;	
PR	14-NOV-1997;	97US-0066029.
XX	14-NOV-1997;	
PA	(AMYL-) AMYLIN PHARM INC.	
XX	(AMYL-) AMYLIN PHARM INC.	

PI Beeley NRA, Prickett KS;
XX
XX WPI; 1999-347456/29.

Peptide agonists of exendin - delay stomach emptying, for treating diabetes and hypo- or hyper-glycaemia

Claim 28; Fig 4; 144pp; English.

XX AA17555 to AA17624 represent exendin peptide agonists. Exendins are
XX peptides that are found in the venom of the Gila-monster, a lizard
XX endogenous to Arizona and Northern Mexico. The peptide agonists are
XX used to treat diabetes mellitus (types I or II), hyperglycaemia or
XX hypoglycaemia. They can also be used for in vitro and in vivo studies
XX on exendins and their agonists. They regulate gastric motility and slow
XX gastric emptying (resulting in lower post-prandial glucose levels).

XX Sequence 37 AA;

Query Match 77.7%; Score 94; DB 20; Length 37;
Best Local Similarity 65.6%; Pred. No. 5.2e-10;
Matches 21; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 4 GTXXXXXSKQEEAVRLXXXXLKNQGSQGA 35
DB 4 GTFSALSQKMEBEAVRLFLEWLKNGGASSGA 35

RESULT 2

AAE08527 ID AAE08527 standard; peptide; 37 AA.

AC AAE08527;

DT 01-NOV-2001 (first entry)

XX Exendin agonist peptide #172.

XX Exendin agonist; antilipemic; cardiac; triglyceride; inotropic;
XX diuretic; coronary heart disease; dyslipidaemia.

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 31 /note= "N-methyl alanine"

FT Modified-site 36 /note= "N-methyl alanine"

FT Modified-site 37 /note= "N-methyl alanine; C-terminal amide"

XX W0200151078-A1.

XX 19-JUL-2001.

XX 09-JAN-2001; 2001WO-US00719.

XX 10-JAN-2000; 2000US-0175365.

XX (AMYL-) AMYLIN PHARM INC.

XX Kolterman OG, Young AA;

XX WPI; 2001-514422/56.

XX Use of exendin and exendin agonist compounds for modulating
XX triglyceride levels, and treating heart disease and dyslipidemia
XX Example 178; Page 143; 161pp; English.

XX The patent discloses a method for modulating plasma or postprandial
XX triglyceride and other lipid levels by administering exendin or an
XX exendin agonist. Exendins have inotropic and diuretic effects. They

CC suppress the secretion of glucagon. Exendin and its agonists have
CC a significant effect on the reduction of blood serum triglyceride
CC concentrations. They are used to treat coronary heart disease and
CC dyslipidaemia, and for modifying postprandial triglyceride levels.
CC The present peptide sequence is an agonist of exendin.

XX Sequence 37 AA;

Query Match 77.7%; Score 94; DB 22; Length 37;
Best Local Similarity 65.6%; Pred. No. 5.2e-10;
Matches 21; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 4 GTXXXXXSKQEEAVRLXXXXLKNQGSQGA 35
DB 4 GTFSALSQKMEBEAVRLFLEWLKNGGASSGA 35

RESULT 3

AAE64363 ID AAE64363 standard; peptide; 37 AA.

AC AAE64363;

DT 27-MAR-2001 (first entry)

XX Exendin agonist, SEQ ID NO:183.

XX Exendin agonist; gestational diabetes mellitus; GDM; insulin resistance;
XX pregnancy complication; neonatal abnormality; blood glucose modulator;
XX insulinotropic; anorectic; exendin-4.

XX Heloderma suspectum.

XX Synthetic.

XX W020007331-A2.

XX 07-DEC-2000.

XX 23-MAY-2000; 2000WO-US14231.

XX 01-JUN-1999; 99US-0323867.

XX (AMYL-) AMYLIN PHARM INC.

XX Hiles R, Prickett KS;

XX WPI; 2001-137634/14.

XX Use of exendins or exendin agonists for lowering or reducing blood
XX glucose levels and treating gestational diabetes mellitus in a subject,
XX especially in a human -
XX Example 178; Page 119; 133pp; English.

XX The invention relates to the use of an exendin (AAE64181-B64182) or
XX an exendin agonist (AAE64185-B64368) for treating gestational diabetes
XX mellitus (GDM) in a patient. GDM arises during pregnancy, and is due
XX to a combination of increased insulin resistance and a diminished
XX ability to increase insulin secretion. In contrast, in a normal
XX pregnancy, both insulin resistance and insulin secretion increase. GDM
XX pregnancies are associated with complications in both the mother and the
XX foetus. Women with GDM have increased rates of Caesarian delivery,
XX hypertensive disorders such as pre-eclampsia, and urinary tract
XX infections. GDM results in an elevated rate of foetal abnormalities such
XX as neural tube defects, and is associated with an increased risk of
XX neonatal morbidities such as hypoglycaemia, hyperbilirubinaemia, and subsequent
XX hypomagnesaemia, polycythaemia, hyperbilirubinaemia, and subsequent
XX childhood and adolescent obesity. Exendins are peptides from the salivary
XX secretions of the Gila monster (exendin-4) and the Mexican beaded lizard
XX (exendin-3) which exhibit homology with several members of the
XX glucagon-like peptide family, particularly GLP-1, and have stimilar
XX insulinotropic effects. Unlike the compounds used to treat type 2
XX diabetes, which are contraindicated for GDM, exendins and exendin

XX 09-AUG-1999 (first entry)
 XX
 DE Exendin agonist peptide #72.
 XX
 XX Exendin; agonist; Heloderma sp.; Gila monster; venom; lizard;
 XX diabetes mellitus type I; diabetes mellitus type II; hyperglycaemia;
 XX hypoglycaemia; plasma glucose; gastric emptying; stomach emptying.
 XX
 OS Synthetic.
 OS Heloderma sp.
 XX
 XX WO9925728-A1.
 XX
 XX 27-MAY-1999.
 XX
 XX 13-NOV-1998; 98WO-US24273.
 XX
 XX 14-NOV-1997; 97US-0066029.
 XX
 XX (AMYL-) AMYLIN PHARM INC.
 XX
 XX Beeley NRA, Prickett KS;
 XX
 XX WPI; 1999-347456/29.
 XX
 XX Peptide agonists of exendin - delay stomach emptying, for treating
 PT diabetes and hypo- or hyper-glycaemia
 XX
 XX Claim 28; Fig 4; 14pp; English.
 XX
 XX
 CC AAY17535 to AAY17624 represent exendin peptide agonists. Exendins are
 CC peptides that are found in the venom of the Gila-monster, a lizard
 CC endogenous to Arizona and Northern Mexico. The peptide agonists are
 CC used to treat diabetes mellitus (types I or II), hyperglycaemia or
 CC hypoglycaemia. They can also be used for in vitro and in vivo studies
 CC on exendins and their agonists. They regulate gastric motility and slow
 CC gastric emptying (resulting in lower post-prandial glucose levels).
 CC
 CC
 SQ Sequence 36 AA;
 SQ
 Query Match 76.9%; Score 93; DB 20; Length 36;
 Best Local Similarity 65.6%; Pred. No. 7.7e-10;
 Matches 21; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
 Oy 4 GTXXXXXXSKOEEAVRLXXXXLKNKGXSSGA 35
 DB 4 GTFTSDASKOLEEAVRLFIETFLKNGSPSSGA 35
 RESULT 7
 AAB11263
 ID AAB11263 standard; Peptide; 36 AA.
 XX
 AC AAB11263;
 XX
 XX 20-FEB-2001 (first entry)
 XX
 DE exendin agonist peptide SEQ ID NO 171.
 XX
 XX Exendin; agonist; treatment; antidiabetic; insulin sensitivity; diabetes;
 XX plasma glucose; gastric emptying; food intake.
 XX
 OS Synthetic.
 OS
 XX WO200041546-A2.
 XX
 XX 20-JUL-2000.
 XX
 XX 10-JAN-2000; 2000US-0116380.
 XX
 XX 14-JAN-1999; 99US-0116380.
 XX

PA (AMYL-) AMYLIN PHARM INC.
 XX
 XX Young A, L'Italien JJ, Kolterman O;
 XX
 XX WPI; 2000-514584/46.
 XX
 XX New formulations comprising an exendin or exendin agonist peptide used
 PT for increasing the sensitivity of a subject to insulin to treat
 PT diabetes -
 XX
 XX Example 180; Page 229; 281pp; English.
 XX
 XX This invention describes a novel formulation (I) comprising an exendin or
 CC exendin agonist peptide, a buffer and an iso-osmolality modifier which
 CC has a pH of 3-7. The products of the invention have antidiabetic
 CC activity. The exendin or exendin agonist is used to increase the
 CC sensitivity of a subject to insulin to treat diabetes and disorders which
 CC would benefit from agents which lower plasma glucose levels and disorders
 CC which would benefit from agents that delay and/or slow gastric emptying
 CC or reducing food intake.
 CC
 CC
 SQ Sequence 36 AA;
 SQ
 Query Match 76.9%; Score 93; DB 21; Length 36;
 Best Local Similarity 65.6%; Pred. No. 7.7e-10;
 Matches 21; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
 Oy 4 GTXXXXXXSKOEEAVRLXXXXLKNKGXSSGA 35
 DB 4 GTFTSDASKOLEEAVRLFIETFLKNGSPSSGA 35
 RESULT 8
 AAB53029
 ID AAB53029 standard; Peptide; 36 AA.
 XX
 AC AAB53029;
 XX
 XX 28-FEB-2001 (first entry)
 XX
 DE Exendin agonist compound #157.
 XX
 XX Exendin; agonist; diabetes; obesity; eating disorder;
 XX dyslipidaemia; insulin-resistance syndrome; food intake.
 XX
 OS Heloderma sp.
 OS
 XX WO200066629-A1.
 XX
 XX 09-NOV-2000.
 XX
 XX 28-APR-2000; 2000WO-US11814.
 XX
 XX 30-APR-1999; 99US-0132018.
 XX
 XX (AMYL-) AMYLIN PHARM INC.
 XX
 XX Young A, Prickett K;
 XX
 XX WPI; 2000-672834/65.
 XX
 XX Modified exendin or an exendin agonist linked to one or more
 PT polyethylene glycol (PEG) polymers, modulate plasma glucose levels,
 PT useful for treating disorders such as diabetes and obesity -
 XX
 XX Disclosure; Fig 4; 119pp; English.
 XX
 XX The present invention relates to extendins and their agonists which have
 CC been modified with molecular weight increasing agents such as
 CC polyethylene glycol (PEG). These can be used in the treatment of
 CC diabetes, obesity, impaired glucose tolerance, postprandial dumping
 CC syndrome, postprandial hyperglycaemia, eating disorders, insulin
 CC resistance syndrome, dyslipidaemia and to suppress glucagon secretion.

XX Sequence 36 AA;

Query Match 76.9%; Score 93; DB 21; Length 36;
 Best Local Similarity 65.6%; Pred. No. 7.7e-10;
 Matches 21; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

4 GTXXXXXXSKQXEENAVRLXXXXLKNGXSSGA 35
 4 GTFTSDASKQLEBEAVRLFIEFLKNGGPSSGA 35

DB

RESULT 9
 AAY94184
 ID AAY94184 standard; peptide; 36 AA.

XX AAY94184;

XX 20-OCT-2000 (first entry)

XX Amino acid sequence of an extendin agonist.

XX Extendin; Gila monster lizard; Mexican Beaded lizard; agonist;

XX glucagon-like peptide; plasma glucagon; necrolytic erythema;

XX glucagonoma; hyperglucagonemia; diabetes.

XX Synthetic.

XX Heloderma sp.

XX Key Location/Qualifiers

XX Modified-site 36

XX /note="amidated residue"

XX WO200041548-A2.

XX 14-JAN-2000; 2000WO-US00942.

XX 14-JAN-1999; 99US-0116380.

XX 30-APR-1999; 99US-0132017.

XX 10-JAN-2000; 2000US-0175365.

XX (AMYL-) AMYLIN PHARM INC.

XX Young A, Gedulin B;

XX WPI; 2000-490999/43.

XX Lowering plasma glucagon using extendin, an extendin agonist, a modified

XX extendin or a modified extendin agonist, useful for treating

XX hyperglucagonemia and diabetes

XX Disclosure; Fig 4G; 96pp; English.

XX The present sequence represents a modified extendin or extendin agonist.

XX Extendins are found in the salivary glands of the Gila monster and

XX Mexican Beaded lizard, and have sequence similarity to glucagon-like

XX peptides. They are used in the method of the invention. The specification

XX describes a method for lowering plasma glucagon, comprising administering

XX an extendin, an extendin agonist, a modified extendin or a modified extendin

XX agonist. These compounds lower plasma glucagon level. The method is

XX useful for lowering plasma glucagon in subjects, preferably humans,

XX suffering from necrolytic erythema or glucagonoma. The method is also

XX useful for treating hyperglucagonemia and other conditions that would

XX benefit from reduced glucagon levels and/or suppression of glucagon,

XX e.g. type 1 and type 2 diabetes.

XX Sequence 36 AA;

XX Query Match 76.9%; Score 93; DB 21; Length 36;

XX Best Local Similarity 65.6%; Pred. No. 7.7e-10;

XX Matches 21; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

4 GTXXXXXXSKQXEENAVRLXXXXLKNGXSSGA 35
 4 GTFTSDASKQLEBEAVRLFIEFLKNGGPSSGA 35

DB

RESULT 10
 AAE08515
 ID AAE08515 standard; peptide; 36 AA.

XX AAE08515;

XX 01-NOV-2001 (first entry)

XX Extendin agonist peptide #160.

XX Extendin agonist; antilipemic; cardiatic; triglyceride; inotropic;

XX diuretic; coronary heart disease; dyslipidaemia.

XX Synthetic.

XX Key Location/Qualifiers

XX Modified-site 36

XX /note="C-terminal amide"

XX WO200151078-A1.

XX 19-JUL-2001.

XX 09-JAN-2001; 2001WO-US00719.

XX 10-JAN-2000; 2000US-0175365.

XX (AMYL-) AMYLIN PHARM INC.

XX Kolterman OG, Young AA;

XX WPI; 2001-514422/56.

XX Use of extendin and extendin agonist compounds for modulating

XX triglyceride levels, and treating heart disease and dyslipidemia

XX Example 166; Page 136; 161pp; English.

XX The patent discloses a method for modulating plasma or postprandial

XX triglyceride and other lipid levels by administering extendin or an

XX extendin agonist. Extendins have inotropic and diuretic effects. They

XX suppress the secretion of glucagon. Extendin and its agonists have

XX a significant effect on the reduction of blood serum triglyceride

XX concentrations. They are used to treat coronary heart disease and

XX dyslipidaemia, and for modifying postprandial triglyceride levels.

XX The present peptide sequence is an agonist of extendin.

XX Sequence 36 AA;

XX Query Match 76.9%; Score 93; DB 22; Length 36;

XX Best Local Similarity 65.6%; Pred. No. 7.7e-10;

XX Matches 21; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

XX 4 GTXXXXXXSKQXEENAVRLXXXXLKNGXSSGA 35

XX 4 GTFTSDASKQLEBEAVRLFIEFLKNGGPSSGA 35

XX Db

XX RESULT 11

XX AAB64351

XX ID AAB64351 standard; peptide; 36 AA.

XX AAB64351;

XX 27-MAR-2001 (first entry)

XX

XX Exendin agonist; gestational diabetes mellitus; GDM; insulin resistance;
 KW pregnancy complication; neonatal abnormality; blood glucose modulator;
 KM insulinotropic; anorectic; exendin-4.

XX Heloderma suspectum.
 OS Synthetic.

XX WO20073331-A2.

XX 07-DEC-2000.

XX 23-MAY-2000; 2000WO-US14231.

XX 01-JUN-1999; 99US-0323867.

XX (AMYL-) AMYLIN PHARM INC.

XX Hiles R, Prickett KS;

XX WPI; 2001-137634/14.

XX Use of exendins or exendin agonists for lowering or reducing blood
 PT glucose levels and treating gestational diabetes mellitus in a subject,
 PT especially in a human -

PS Example 166; Page 113; 133pp; English.

XX The invention relates to the use of an exendin (AAB64181-B64182) or
 CC an exendin agonist (AAB64185-B64368) for treating gestational diabetes
 CC mellitus (GDM) in a patient. GDM arises during pregnancy, and is due
 CC to a combination of increased insulin resistance and a diminished
 CC ability to increase insulin secretion. In contrast, in a normal
 CC pregnancy, both insulin resistance and insulin secretion increase. GDM
 CC pregnancies are associated with complications in both the mother and the
 CC foetus. Women with GDM have increased rates of Caesarian delivery,
 CC hypertensive disorders such as pre-eclampsia, and urinary tract
 CC infections. GDM results in an elevated rate of foetal abnormalities such
 CC as neural tube defects, and is associated with an increased risk of
 CC neonatal morbidities such as hypoglycaemia, hypocalcaemia, and subsequent
 CC hypomagnesaemia, polycythaemia, hyperbilirubinaemia, and subsequent
 CC childhood and adolescent obesity. Exendins are peptides from the gallvary
 CC secretions of the Gila monster (exendin-4) and the Mexican beaded lizard
 CC (exendin-3) which exhibit homology with several members of the
 CC glucagon-like peptide family, particularly GLP-1, and have similar
 CC insulinotropic effects. Unlike the compounds used to treat type 2
 CC diabetes, which are contraindicated for GDM, exendins and exendin
 CC agonists do not cross the placenta and thus do not cause severe prolonged
 CC hypoglycaemia in the newborn. They have a potent and prolonged effect on
 CC blood glucose, and, unlike conventional insulin therapy, should not cause
 CC weight gain, as they inhibit gastric emptying and reduce appetite. The
 CC present sequence represents an exendin agonist of the invention which is
 CC based upon the sequence of exendin-4.

XX Sequence 36 AA;

Query Match 76.9%; Score 93; DB 22; Length 36;
 Best Local Similarity 65.6%; Pred. No. 7.7e-10;
 Matches 21; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 4 GTXXXXXKXKEEAVRLXXXXLXNGXSXSGA 35
 |||||
 DB 4 GTFTSDASKQLEEAVALFLFLEFLKNGXSSGA 35

RESULT 12
 AAY24869 standard; peptide; 37 AA.

XX AAY24869;

XX 24-AUG-1999 (first entry)

DE Exendin agonist peptide #61.

XX Exendin; agonist; Heloderma sp.; Gila monster; venom; lizard;
 KW diabetes mellitus type I; diabetes mellitus type II; hyperglycaemia;
 KM hypoglycaemia; plasma glucose; gastric emptying; stomach emptying.

XX Synthetic.

XX Heloderma sp.

XX WO9925727-A2.

XX 27-MAY-1999.

XX 13-NOV-1998; 98WO-US624210.

XX 14-NOV-1997; 97US-0065442.

XX (AMYL-) AMYLIN PHARM INC.

XX Bealey NRA, Prickett KS;

XX WPI; 1999-394773/33.

XX New exendin agonist peptides - can regulate gastric motility and
 PT slow gastric emptying, used for treating, e.g. diabetes
 PT Claim 18; Fig 4; 108pp; English.

XX AAY24809 to AAY24877 represent exendin agonist peptides which can
 CC regulate gastric motility and slow gastric emptying. The peptides can be
 CC used for treating e.g. diabetes or hyperglycaemic or hypoglycaemic
 CC conditions. The peptides are exendin agonists which have activity as
 CC agents to regulate gastric motility and to slow gastric emptying, as
 CC evidenced by the ability to reduce post-prandial glucose levels in
 CC mammals. They can be used for the treatment of Type I and II diabetes and
 CC hyperglycaemic or hypoglycaemic conditions. They can also be used for the
 CC treatment of disorders which would be benefited by agents which lower
 CC plasma glucose levels and in treatment of disorders which would be
 CC benefited with agents useful in delaying and/or slowing gastric
 CC emptying.

XX Sequence 37 AA;

Query Match 76.9%; Score 93; DB 20; Length 37;
 Best Local Similarity 68.8%; Pred. No. 8e-10;
 Matches 22; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 4 GTXXXXXKXKEEAVRLXXXXLXNGXSXSGA 35
 |||||
 DB 4 GTFTSDASKQMEEAVALFLFLEWLKNGXSXSGA 35

RESULT 13

AAY24853 standard; peptide; 37 AA.

XX AAY24853;

XX 24-AUG-1999 (first entry)

XX Exendin agonist peptide #45.

XX Exendin; agonist; Heloderma sp.; Gila monster; venom; lizard;
 KW diabetes mellitus type I; diabetes mellitus type II; hyperglycaemia;
 KM hypoglycaemia; plasma glucose; gastric emptying; stomach emptying.

XX Synthetic.

XX Heloderma sp.

XX WO9925727-A2.

XX 27-MAY-1999.

Best Local Similarity 68.8%; Pred. No. 8e-10;
Matches 22; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 4 GTXXXXXSKQKEEAVRLXXXXLKNKGXSSGA 35
4 GTFTSALSQKQEEAVRLFIEWLKNKGXSSGA 35

RESULT 16
AAB53041
ID AAB53041 standard; Peptide; 37 AA.

AC AAB53041;

DT 28-FEB-2001 (first entry)

DE Extendin agonist compound #169.

KW Extendin; agonist; diabetes; obesity; eating disorder;
dyslipidaemia; insulin-resistance syndrome; food intake.

OS Heloderma sp.

PN W0200066629-A1.

PD 09-NOV-2000.

PF 28-APR-2000; 2000WO-US11814.

PR 30-APR-1999; 99US-0132018.

PA (AMYL-) AMYLIN PHARM INC.

PI Young A, Prickett K;

DR WPI: 2000-672834/65.

XX Modified extendin or an extendin agonist linked to one or more

PT polyethylene glycol (PEG) polymers, modulate plasma glucose levels,

PS useful for treating disorders such as diabetes and obesity -

XX Disclosure; Fig 4; 11pp; English.

CC The present invention relates to extendins and their agonists which have

CC been modified with molecular weight increasing agents such as

CC polyethylene glycol (PEG). These can be used in the treatment of

CC diabetes, obesity, impaired glucose tolerance, postprandial dumping

CC syndrome, postprandial hyperglycaemia, eating disorders, insulin

CC resistance syndrome, dyslipidaemia and to suppress glucagon secretion.

CC Sequence 37 AA;

QY 4 GTXXXXXSKQKEEAVRLXXXXLKNKGXSSGA 35

DB 4 GTFTSALSQKQEEAVRLFIEWLKNKGXSSGA 35

AA94196

ID AAY94196 standard; peptide; 37 AA.

AC AAY94196;

DT 20-OCT-2000 (first entry)

DE Amino acid sequence of an extendin agonist.

XX Extendin; Gila monster lizard; Mexican Beaded lizard; agonist;
KW glucagon-like peptide; plasma glucagon; necrolytic erythema;

KW glucagonoma; hyperglucagonemia; diabetes.

OS Synthetic.

OS Heloderma sp.

FT Key Location/Qualifiers

FT Modified-site 31 /note= "N-methyl alanine"

FT Modified-site 35 /note= "N-methyl alanine"

FT Modified-site 37 /note= "N-methyl alanine"

FT Modified-site 38 /note= "amidated N-methyl alanine"

FT W0200041548-A2.

PN 20-JUL-2000.

PF 14-JAN-2000; 2000WO-US00942.

PR 14-JAN-1999; 99US-0116380.

PR 30-APR-1999; 99US-0132017.

PR 10-JAN-2000; 2000US-0175365.

PA (AMYL-) AMYLIN PHARM INC.

PI Young A, Gedulin B;

DR WPI: 2000-490999/43.

XX Lowering plasma glucagon using extendin, an extendin agonist, a modified

PT extendin or a modified extendin agonist, useful for treating

PS hyperglucagonemia and diabetes -

XX Disclosure; Fig 4G; 96pp; English.

CC The present sequence represents a modified extendin or extendin agonist.

CC Extendins are found in the salivary glands of the Gila monster and

CC Mexican Beaded lizard, and have sequence similarity to glucagon-like

CC peptides. They are used in the method of the invention. The specification

CC describes a method for lowering plasma glucagon, comprising administering

CC an extendin, an extendin agonist, a modified extendin or a modified

CC agonist. These compounds lower plasma glucagon level. The method is

CC useful for lowering plasma glucagon in subjects, preferably humans,

CC suffering from necrolytic erythema or glucagonoma. The method is also

CC useful for treating hyperglucagonemia and other conditions that would

CC benefit from reduced glucagon levels and/or suppression of glucagon.

CC e.g. type 1 and type 2 diabetes.

CC Sequence 37 AA;

QY 4 GTXXXXXSKQKEEAVRLXXXXLKNKGXSSGA 35

DB 4 GTFTSALSQKQEEAVRLFIEWLKNKGXSSGA 35

AAE08427

ID AAE08427 standard; peptide; 37 AA.

AC AAE08427;

DT 01-NOV-2001 (first entry)

DE Extendin agonist peptide #72.

XX Extendin agonist; antilipemic; cardiac; triglyceride; inotropic;
KW diuretic; coronary heart disease; dyslipidaemia.

XX OS Synthetic.
XX Key Location/Qualifiers
XX FT Modified-site 31
XX FT /note= "N-Methyl-alanine"
XX FT Modified-site 37
XX FT /note= "C-terminal amide"
XX PN WO200151078-A1.
XX PD 19-JUL-2001.
XX PF 09-JAN-2001; 2001WO-US00719.
XX PR 10-JAN-2000; 2000US-0175365.
XX PA (AMYL-) AMYLIN PHARM INC.
XX PI Kolterman OG, Young AA;
XX DR WPI; 2001-514422/56.
XX XX
XX PT Use of exendin and exendin agonist compounds for modulating
XX PT triglyceride levels, and treating heart disease and dyslipidemia
XX PS Example 76; Page 82; 161pp; English.
XX CC The patent discloses a method for modulating plasma or postprandial
XX CC triglyceride and other lipid levels by administering exendin or an
XX CC exendin agonist. Exendins have inotropic and diuretic effects. They
XX CC suppress the secretion of glucagon. Exendin and its agonists have
XX CC a significant effect on the reduction of blood serum triglyceride
XX CC concentrations. They are used to treat coronary heart disease and
XX CC dyslipidaemia, and for modifying postprandial triglyceride levels.
XX CC The present peptide sequence is an agonist of exendin.
XX CC
XX SQ Sequence 37 AA;
XX
XX Query Match 76.9%; Score 93; DB 22; Length 37;
XX Best Local Similarity 65.6%; Pred. No. 8e-10;
XX Matches 21; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
XX
XX QY 4 GTXXXXXXSKOXEBAVRLXXXXLKNKGXSSGA 35
XX |||||
XX 4 GTFTSDLSKOMBEBAVRLFIEMLNKGASGSA 35
XX DB
XX
XX RESULT 19
XX ID AAE08428
XX AAE08428 standard; peptide; 37 AA.
XX
XX AC AAE08428;
XX
XX DT 01-NOV-2001 (first entry)
XX
XX DE Exendin agonist peptide #73.
XX
XX KM Exendin agonist; antilipemic; cardiast; triglyceride; inotropic;
XX KM diuretic; coronary heart disease; dyslipidaemia.
XX
XX OS Synthetic.
XX
XX Key Location/Qualifiers
XX FH Modified-site 31
XX FT /note= "N-Methyl-alanine"
XX FT Modified-site 36
XX FT /note= "N-Methyl-alanine"
XX FT Modified-site 37
XX FT /note= "N-Methyl-alanine; C-terminal amide"
XX PN WO200151078-A1.
XX DR

PD 19-JUL-2001.
XX XX
XX PF 09-JAN-2001; 2001WO-US00719.
XX PR 10-JAN-2000; 2000US-0175365.
XX PA (AMYL-) AMYLIN PHARM INC.
XX PI Kolterman OG, Young AA;
XX DR WPI; 2001-514422/56.
XX XX
XX PT Use of exendin and exendin agonist compounds for modulating
XX PT triglyceride levels, and treating heart disease and dyslipidemia
XX PS Example 77; Page 83; 161pp; English.
XX CC The patent discloses a method for modulating plasma or postprandial
XX CC triglyceride and other lipid levels by administering exendin or an
XX CC exendin agonist. Exendins have inotropic and diuretic effects. They
XX CC suppress the secretion of glucagon. Exendin and its agonists have
XX CC a significant effect on the reduction of blood serum triglyceride
XX CC concentrations. They are used to treat coronary heart disease and
XX CC dyslipidaemia, and for modifying postprandial triglyceride levels.
XX CC The present peptide sequence is an agonist of exendin.
XX CC
XX SQ Sequence 37 AA;
XX
XX Query Match 76.9%; Score 93; DB 22; Length 37;
XX Best Local Similarity 65.6%; Pred. No. 8e-10;
XX Matches 21; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
XX
XX QY 4 GTXXXXXXSKOXEBAVRLXXXXLKNKGXSSGA 35
XX |||||
XX 4 GTFTSDLSKOMBEBAVRLFIEMLNKGASGSA 35
XX DB
XX
XX RESULT 20
XX ID AAE08443
XX AAE08443 standard; peptide; 37 AA.
XX
XX AC AAE08443;
XX
XX DT 01-NOV-2001 (first entry)
XX
XX DE Exendin agonist peptide #88.
XX
XX KM Exendin agonist; antilipemic; cardiast; triglyceride; inotropic;
XX KM diuretic; coronary heart disease; dyslipidaemia.
XX
XX OS Synthetic.
XX
XX Key Location/Qualifiers
XX FH Modified-site 31
XX FT /note= "Homoproline"
XX FT Modified-site 36
XX FT /note= "Homoproline"
XX FT Modified-site 37
XX FT /note= "Homoproline; C-terminal amide"
XX PN WO200151078-A1.
XX PD 19-JUL-2001.
XX PF 09-JAN-2001; 2001WO-US00719.
XX PR 10-JAN-2000; 2000US-0175365.
XX PA (AMYL-) AMYLIN PHARM INC.
XX PI Kolterman OG, Young AA;
XX DR WPI; 2001-514422/56.
XX

XX Use of exendin and exendin agonist compounds for modulating
PT triglyceride levels, and treating heart disease and dyslipidemia
XX
XX Example 92; Page 92; 161pp; English.
XX The patent discloses a method for modulating plasma or postprandial
CC triglyceride and other lipid levels by administering exendin or an
CC exendin agonist. Exendins have inotropic and diuretic effects. They
CC suppress the secretion of glucagon. Exendin and its agonists have
CC a significant effect on the reduction of blood serum triglyceride
CC concentrations. They are used to treat coronary heart disease and
CC dyslipidaemia, and for modifying postprandial triglyceride levels.
CC The present peptide sequence is an agonist of exendin.
SQ Sequence 37 AA;
XX
XX Query Match 76.9%; Score 93; DB 22; Length 37;
Best Local Similarity 68.8%; Pred. No. 8e-10;
Matches 22; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 4 GTXXXXXXSKXEEAVRLXXXXLKNKGXSSGA 35
DB 4 GTFTSDLSKXMEAEAVRLFIEWLKNGXSSGA 35
RESULT 21
AAB64263 standard; peptide; 37 AA.
ID AAB64263
XX AAB64263;
XX AC
XX 27-MAR-2001 (first entry)
XX DT
XX DE Exendin agonist, SEQ ID NO:83.
XX KM Exendin agonist; gestational diabetes mellitus; GDM; insulin resistance;
XX KM pregnancy complication; neonatal abnormality; blood glucose modulator;
XX KM insulinotropic; anorectic; exendin-4.
XX OS Heloderma suspectum.
XX OS Synthetic.
XX PN WO200073331-A2.
XX PD 07-DEC-2000.
XX PF 23-MAY-2000; 2000WO-US14231.
XX PR 01-JUN-1999; 99US-0323867.
XX PA (AMYL-) AMYLIN PHARM INC.
XX PI Hiles R, Prickett KS;
XX PI WPI; 2001-137634/14.
XX DR
XX PT Use of exendin or exendin agonists for lowering or reducing blood
PT glucose levels and treating gestational diabetes mellitus in a subject,
PT especially in a human -
XX
XX Example 76; Page 67; 133pp; English.
XX The invention relates to the use of an exendin (AAB64181-B64182) or
CC an exendin agonist (AAB64185-B64368) for treating gestational diabetes
CC mellitus (GDM) in a patient. GDM arises during pregnancy, and is due
CC to a combination of increased insulin resistance and a diminished
CC ability to increase insulin secretion. In contrast, in a normal
CC pregnancy, both insulin resistance and insulin secretion increase. GDM
CC pregnancies are associated with complications in both the mother and the
CC foetus. Women with GDM have increased rates of Caesarian delivery,
CC hypertensive disorders such as pre-eclampsia, and urinary tract
CC infections. GDM results in an elevated rate of foetal abnormalities such

CC as neural tube defects, and is associated with an increased risk of
CC neonatal morbidities such as hypoglycaemia, hypocalcaemia,
CC hypomagnesaemia, polycythaemia, hyperbilirubinemia, and subsequent
CC childhood and adolescent obesity. Exendins are peptides from the salivary
CC secretions of the Gila monster (exendin-4) and the Mexican beaded lizard
CC (exendin-3) which exhibit homology with several members of the
CC glucagon-like peptide family, particularly GLP-1, and have similar
CC insulinotropic effects. Unlike the compounds used to treat type 2
CC diabetes, which are contraindicated for GDM, exendins and exendin
CC agonists do not cross the placenta and thus do not cause severe prolonged
CC hypoglycaemia in the newborn. They have a potent and prolonged effect on
CC blood glucose, and, unlike conventional insulin therapy, should not cause
CC weight gain, as they inhibit gastric emptying and reduce appetite. The
CC present sequence represents an exendin agonist of the invention which is
CC based upon the sequence of exendin-4.
XX
XX SQ Sequence 37 AA;
XX
XX Query Match 76.9%; Score 93; DB 22; Length 37;
Best Local Similarity 65.6%; Pred. No. 8e-10;
Matches 21; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
QY 4 GTXXXXXXSKXEEAVRLXXXXLKNKGXSSGA 35
DB 4 GTFTSDLSKXMEAEAVRLFIEWLKNGXSSGA 35
RESULT 22
AAB64264 standard; peptide; 37 AA.
ID AAB64264
XX AAB64264;
XX AC
XX 27-MAR-2001 (first entry)
XX DT
XX DE Exendin agonist, SEQ ID NO:84.
XX KM Exendin agonist; gestational diabetes mellitus; GDM; insulin resistance;
XX KM pregnancy complication; neonatal abnormality; blood glucose modulator;
XX KM insulinotropic; anorectic; exendin-4.
XX OS Heloderma suspectum.
XX OS Synthetic.
XX PN WO200073331-A2.
XX PD 07-DEC-2000.
XX PF 23-MAY-2000; 2000WO-US14231.
XX PR 01-JUN-1999; 99US-0323867.
XX PA (AMYL-) AMYLIN PHARM INC.
XX PI Hiles R, Prickett KS;
XX PI WPI; 2001-137634/14.
XX DR
XX PT Use of exendins or exendin agonists for lowering or reducing blood
PT glucose levels and treating gestational diabetes mellitus in a subject,
PT especially in a human -
XX
XX Example 77; Page 68; 133pp; English.
XX The invention relates to the use of an exendin (AAB64181-B64182) or
CC an exendin agonist (AAB64185-B64368) for treating gestational diabetes
CC mellitus (GDM) in a patient. GDM arises during pregnancy, and is due
CC to a combination of increased insulin resistance and a diminished
CC ability to increase insulin secretion. In contrast, in a normal
CC pregnancy, both insulin resistance and insulin secretion increase. GDM
CC pregnancies are associated with complications in both the mother and the
CC foetus. Women with GDM have increased rates of Caesarian delivery,
CC hypertensive disorders such as pre-eclampsia, and urinary tract

infections. GDM results in an elevated rate of foetal abnormalities such as neural tube defects, and is associated with an increased risk of neonatal morbidities such as hypoglycaemia, hypocalcaemia, and subsequent hypomagnesaemia, polycythaemia, hyperbilirubinaemia, and subsequent childhood and adolescent obesity. Exendins are peptides from the salivary secretions of the Gila monster (exendin-4) and the Mexican beaded lizard (exendin-3) which exhibit homology with several members of the glucagon-like peptide family, particularly GLP-1, and have similar insulinotropic effects. Unlike the compounds used to treat type 2 diabetes, which are contraindicated for GDM, exendins and exendin agonists do not cross the placenta and thus do not cause severe prolonged hypoglycaemia in the newborn. They have a potent and prolonged effect on blood glucose, and, unlike conventional insulin therapy, should not cause weight gain, as they inhibit gastric emptying and reduce appetite. The present sequence represents a exendin agonist of the invention which is based upon the sequence of exendin-4.

Sequence 37 AA:
Query Match 76.9%; Score 93; DB 22; Length 37;
Best Local Similarity 65.6%; Pred. No. 8e-10; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 11;

4 GTXXXXXSKQEEAVRLXXXXLKNQXSSGA 35
4 GTFTSDLSKQMEBAVRLFTLWLNQXGSSGA 35

RESULT 23

AAB64279
ID AAB64279 standard; peptide; 37 AA.

AC AAB64279;

DT 27-MAR-2001 (first entry)

DE Exendin agonist, SEQ ID NO:99.

KM Exendin agonist; gestational diabetes mellitus; GDM; insulin resistance; pregnancy complication; neonatal abnormality; blood glucose modulator; insulinotropic; anorectic; exendin-4.

OS Heloderma suspectum.

OS Synthetic.

PN WO200073331-A2.

PD 07-DEC-2000.

PF 23-MAY-2000; 2000WO-US14231.

PR 01-JUN-1999; 99US-0323867.

PA (AMYL-) AMYLIN PHARM INC.

PI Hiles R, Prickett KS;

DR WPI; 2001-137634/14.

PT Use of exendins or exendin agonists for lowering or reducing blood glucose levels and treating gestational diabetes mellitus in a subject, especially in a human -

PS Example 92; Page 75; 133pp; English.

CC The invention relates to the use of an exendin (AAB64181-B64182) or an exendin agonist (AAB64185-B64368) for treating gestational diabetes mellitus (GDM) in a patient. GDM arises during pregnancy, and is due to a combination of increased insulin resistance and a diminished ability to increase insulin secretion. In contrast, in a normal pregnancy, both insulin resistance and insulin secretion increase. GDM pregnancies are associated with complications in both the mother and the foetus. Women with GDM have increased rates of Caesarian delivery.

hypertensive disorders such as pre-eclampsia, and urinary tract infections. GDM results in an elevated rate of foetal abnormalities such as neural tube defects, and is associated with an increased risk of neonatal morbidities such as hypoglycaemia, hypocalcaemia, and subsequent hypomagnesaemia, polycythaemia, hyperbilirubinaemia, and subsequent childhood and adolescent obesity. Exendins are peptides from the salivary secretions of the Gila monster (exendin-4) and the Mexican beaded lizard (exendin-3) which exhibit homology with several members of the glucagon-like peptide family, particularly GLP-1, and have similar insulinotropic effects. Unlike the compounds used to treat type 2 diabetes, which are contraindicated for GDM, exendins and exendin agonists do not cross the placenta and thus do not cause severe prolonged hypoglycaemia in the newborn. They have a potent and prolonged effect on blood glucose, and, unlike conventional insulin therapy, should not cause weight gain, as they inhibit gastric emptying and reduce appetite. The present sequence represents a exendin agonist of the invention which is based upon the sequence of exendin-4.

Sequence 37 AA:
Query Match 76.9%; Score 93; DB 22; Length 37;
Best Local Similarity 68.8%; Pred. No. 8e-10; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 10;

4 GTXXXXXSKQEEAVRLXXXXLKNQXSSGA 35
4 GTFTSDLSKQMEBAVRLFTLWLNQXGSSGA 35

RESULT 24

AAB11311
ID AAB11311 standard; Peptide; 39 AA.

AC AAB11311;

DT 20-FEB-2001 (first entry)

DE exendin agonist peptide SEQ ID NO 37.

KM Exendin; agonist; treatment; antidiabetic; insulin sensitivity; diabetes; plasma glucose; gastric emptying; food intake.

OS Synthetic.

OS WO200041546-A2.

PD 20-JUL-2000.

PF 10-JAN-2000; 2000US-0116380.

PR 14-JAN-1999; 99US-0116380.

PA (AMYL-) AMYLIN PHARM INC.

PI Young A, L'Italien JT, Kolterman O;

DR WPI; 2000-514584/46.

PT New formulations comprising an exendin or exendin agonist peptide used for increasing the sensitivity of a subject to insulin to treat diabetes -

PS Example 42; Figure 15; 281pp; English.

CC This invention describes a novel formulation (I) comprising an exendin or exendin agonist peptide, a buffer and an iso-osmolality modifier which has a pH of 3-7. The products of the invention have antidiabetic activity. The exendin or exendin agonist is used to increase the sensitivity of a subject to insulin to treat diabetes and disorders which would benefit from agents which lower plasma glucose levels and disorders which would benefit from agents that delay and/or slow gastric emptying or reducing food intake.

SQ Sequence 39 AA;
Query Match 76.9%; Score 93; DB 21; Length 39;
Best Local Similarity 65.6%; Pred. No. 8.5e-10;
Matches 21; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
QY 4 GTXXXXXSKQEEAVRLXXXXLXNGXSSGA 35
4 GTFTDLSKQMBEAVRLFIEFLKNGXSSGA 35
Db 4 GTFTDLSKQMBEAVRLFIEFLKNGXSSGA 35

RESULT 25
AA94039
ID AA94039 standard; peptide: 39 AA.
XX
AC AA94039;
XX
DT 20-OCT-2000 (first entry)
XX
DE Amino acid sequence of an extendin agonist.
XX
KW Extendin; Gila monster lizard; Mexican Beaded lizard; agonist;
KW glucagon-like peptide; plasma glucagon; necrolytic erythema;
KW glucagonoma; hyperglucagonemia; diabetes.
XX
OS Synthetic.
OS Heloderma sp.
XX
FH Key Location/Qualifiers
FT Modified-site 31 /note= "thioprolin"
FT Modified-site 36 /note= "thioprolin"
FT Modified-site 37 /note= "thioprolin"
FT Modified-site 38 /note= "thioprolin"
FT Modified-site 38 /note= "thioprolin"
XX
PN MO200041548-A2.
XX
PD 20-JUL-2000.
XX
PF 14-JAN-2000; 2000MO-US00942.
XX
PR 14-JAN-1999; 99US-0116380.
PR 30-APR-1999; 99US-0132017.
PR 10-JAN-2000; 2000US-0175365.
XX
PA (AMYL-) AMYLIN PHARM INC.
XX
PI Young A, Gedulin B;
XX
DR WPI; 2000-490999/43.
XX
PT Lowering plasma glucagon using extendin, an extendin agonist, a modified
PT extendin or a modified extendin agonist, useful for treating
PT hyperglucagonemia and diabetes -
XX
PS Disclosure; Fig 3B; 96pp; English.
XX
AA94013-43 represent extendin agonists, derived from AA94012.
XX
CC Extendins are found in the salivary glands of the Gila monster and
CC Mexican Beaded lizard, and have sequence similarity to glucagon-like
CC peptides. They are used in the method of the invention. The specification
CC describes a method for lowering plasma glucagon, comprising administering
CC an extendin, an extendin agonist, a modified extendin or a modified extendin
CC agonist. These compounds lower plasma glucagon level. The method is
CC useful for lowering plasma glucagon in subjects, preferably humans,
CC suffering from necrolytic erythema or glucagonoma. The method is also
CC useful for treating hyperglucagonemia and other conditions that would
CC benefit from reduced glucagon levels and/or suppression of glucagon,
CC e.g. type 1 and type 2 diabetes.
XX

SQ Sequence 39 AA;
Query Match 76.9%; Score 93; DB 21; Length 39;
Best Local Similarity 68.8%; Pred. No. 8.5e-10;
Matches 22; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 4 GTXXXXXSKQEEAVRLXXXXLXNGXSSGA 35
4 GTFTDLSKQMBEAVRLFIEFLKNGXSSGA 35
Db 4 GTFTDLSKQMBEAVRLFIEFLKNGXSSGA 35

RESULT 26
AA94040
ID AA94040 standard; peptide: 39 AA.
XX
AC AA94040;
XX
DT 20-OCT-2000 (first entry)
XX
DE Amino acid sequence of an extendin agonist.
XX
KW Extendin; Gila monster lizard; Mexican Beaded lizard; agonist;
KW glucagon-like peptide; plasma glucagon; necrolytic erythema;
KW glucagonoma; hyperglucagonemia; diabetes.
XX
OS Synthetic.
OS Heloderma sp.
XX
FH Key Location/Qualifiers
FT Modified-site 31 /note= "homoprolin"
FT Modified-site 36 /note= "homoprolin"
FT Modified-site 37 /note= "homoprolin"
FT Modified-site 38 /note= "homoprolin"
FT Modified-site 38 /note= "homoprolin"
XX
PN MO200041548-A2.
XX
PD 20-JUL-2000.
XX
PF 14-JAN-2000; 2000MO-US00942.
XX
PR 14-JAN-1999; 99US-0116380.
PR 30-APR-1999; 99US-0132017.
PR 10-JAN-2000; 2000US-0175365.
XX
PA (AMYL-) AMYLIN PHARM INC.
XX
PI Young A, Gedulin B;
XX
DR WPI; 2000-490999/43.
XX
PT Lowering plasma glucagon using extendin, an extendin agonist, a modified
PT extendin or a modified extendin agonist, useful for treating
PT hyperglucagonemia and diabetes -
XX
PS Disclosure; Fig 3B; 96pp; English.
XX
AA94013-43 represent extendin agonists, derived from AA94012.
XX
CC Extendins are found in the salivary glands of the Gila monster and
CC Mexican Beaded lizard, and have sequence similarity to glucagon-like
CC peptides. They are used in the method of the invention. The specification
CC describes a method for lowering plasma glucagon, comprising administering
CC an extendin, an extendin agonist, a modified extendin or a modified extendin
CC agonist. These compounds lower plasma glucagon level. The method is
CC useful for lowering plasma glucagon in subjects, preferably humans,
CC suffering from necrolytic erythema or glucagonoma. The method is also
CC useful for treating hyperglucagonemia and other conditions that would
CC benefit from reduced glucagon levels and/or suppression of glucagon,
CC e.g. type 1 and type 2 diabetes.
XX

SQ Sequence 39 AA;
Query Match 76.9%; Score 93; DB 21; Length 39;
Best Local Similarity 68.8%; Pred. No. 8.5e-10;
Matches 22; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
4 GTXXXXXXSKOXEEAVRLXXXXLKNKGXSSGA 35
4 GTFTSDLSKQLEBAVRLFTFPLKNKGXSSGA 35

RESULT 27
AA94043
ID AAY94043 standard; peptide; 39 AA.

AC AAY94043;
DT 20-OCT-2000 (first entry)
DE Amino acid sequence of an extendin agonist.

XX Extendin; Gila monster lizard; Mexican Beaded lizard; agonist;
KM glucagon-like peptide; plasma glucagon; necrolytic erythema;
KW glucagonoma; hyperglucagonemia; diabetes.

XX Synthetic.
OS Heloderma sp.

XX Key Location/Qualifiers
FT Modified-site 31 /note= "N-methylalanine"
FT Modified-site 36 /note= "N-methylalanine"
FT Modified-site 37 /note= "N-methylalanine"
FT Modified-site 38 /note= "N-methylalanine"
FT Modified-site 38 /note= "N-methylalanine"

XX MO200041548-A2.

XX 20-JUL-2000.

XX 14-JAN-2000; 2000WO-US00942.

XX 14-JAN-1999; 99US-0116380.

XX 30-APR-1999; 99US-0132017.

XX 10-JAN-2000; 2000US-0175365.

XX (AMYL-) AMYLIN PHARM INC.

XX Young A. Gedulin B;

XX WPI; 2000-490999/43.

XX Lowering plasma glucagon using extendin, an extendin agonist, a modified
PT extendin or a modified extendin agonist, useful for treating
PS hyperglucagonemia and diabetes -
XX Disclosure; Fig B; 96pp; English.

XX AAY94013-43 represent extendin agonists, derived from AAY94012.
CC Extending are found in the salivary glands of the Gila monster and
CC Mexican Beaded lizard, and have sequence similarity to glucagon-like
CC peptides. They are used in the method of the invention. The specification
CC describes a method for lowering plasma glucagon, comprising administering
CC an extendin, an extendin agonist, a modified extendin or a modified
CC agonist. These compounds lower plasma glucagon level. The method is
CC useful for lowering plasma glucagon in subjects, preferably humans,
CC suffering from necrolytic erythema or glucagonoma. The method is also
CC useful for treating hyperglucagonemia and other conditions that would
CC benefit from reduced glucagon levels and/or suppression of glucagon.
CC e.g. type 1 and type 2 diabetes.

SQ Sequence 39 AA;
Query Match 76.9%; Score 93; DB 21; Length 39;
Best Local Similarity 68.8%; Pred. No. 8.5e-10;
Matches 22; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
4 GTXXXXXXSKOXEEAVRLXXXXLKNKGXSSGA 35
4 GTFTSDLSKQLEBAVRLFTFPLKNKGXSSGA 35

RESULT 28
AAE08379
ID AAE08379 standard; peptide; 39 AA.

AC AAE08379;

DT 01-NOV-2001 (first entry)

DE Extendin agonist peptide #26.

XX Extendin agonist; antilipemic; cardiac; triglyceride; inotropic;
KM diuretic; coronary heart disease; dyslipidaemia.
KW Synthetic.

XX Key Location/Qualifiers
FT Modified-site 31 /note= "Thioprolin"
FT Modified-site 36 /note= "Thioprolin"
FT Modified-site 37 /note= "Thioprolin"
FT Modified-site 38 /note= "Thioprolin"
FT Modified-site 39 /note= "Thioprolin"
FT Modified-site 39 /note= "C-terminal amide"

XX MO200151078-A1.

XX 19-JUL-2001.

XX 09-JAN-2001; 2001WO-US00719.

XX 10-JAN-2000; 2000US-0175365.

XX (AMYL-) AMYLIN PHARM INC.

XX Kolterman OG, Young AA;

XX WPI; 2001-514422/56.

XX Use of extendin and extendin agonist compounds for modulating
PT triglyceride levels, and treating heart disease and dyslipidemia -
XX Example 26; Page -; 161pp; English.

XX The patent discloses a method for modulating plasma or postprandial
CC triglyceride and other lipid levels by administering extendin or an
CC extendin agonist. Extendin has inotropic and diuretic effects. They
CC suppress the secretion of glucagon. Extendin and its agonists have
CC a significant effect on the reduction of blood serum triglyceride
CC concentrations. They are used to treat coronary heart disease and
CC dyslipidaemia, and for modifying postprandial triglyceride levels.
CC Note: The present peptide sequence is an agonist of extendin.
CC derived from SEQ ID NO:3 shown in page 17 of the specification.

QY 4 GTXXXXXSKQEEAVRLXXXXLKNKGXSSGA 35
ID AAE08381
DB 4 GTFTSDLSKQLEEAVALRFLFELKNGXSSGA 35

RESULT 29

AAE08380 standard; peptide; 39 AA.

AC AAE08380;
DT 01-NOV-2001 (first entry)
DE Exendin agonist peptide #27.

XX Exendin agonist; antilipemic; cardiatic; triglyceride; inotropic;
KM diuretic; coronary heart disease; dyslipidaemia.
XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 31 /note= "Homopropine"

FT Modified-site 36 /note= "Homopropine"

FT Modified-site 37 /note= "Homopropine"

FT Modified-site 38 /note= "Homopropine"

FT Modified-site 39 /note= "Homopropine"

FT Modified-site 39 /note= "C-terminal amide"

PN W0200151078-A1.

PD 19-JUL-2001.

PF 09-JAN-2001; 2001WO-US00719.

PR 10-JAN-2000; 2000US-0175365.

PA (AMYL-) AMYLIN PHARM INC.

PI Kolterman OG, Young AA;

XX WPI; 2001-514422/56.

DR WPI; 2001-514422/56.

XX Use of exendin and exendin agonist compounds for modulating

PT triglyceride levels, and treating heart disease and dyslipidemia

XX Example 27; Page -; 161pp; English.

XX The patent discloses a method for modulating plasma or postprandial

CC triglyceride and other lipid levels by administering exendin or an

CC exendin agonist. Exendins have inotropic and diuretic effects. They

CC suppress the secretion of glucagon. Exendin and its agonists have

CC a significant effect on the reduction of blood serum triglyceride

CC concentrations. They are used to treat coronary heart disease and

CC dyslipidaemia, and for modifying postprandial triglyceride levels.

CC Note: The present peptide sequence is an agonist of exendin.

CC Note: The present sequence is not shown in the specification but is

CC derived from SEQ ID NO.3 shown in page 17 of the specification.

XX Sequence 39 AA;

XX Query Match 76.9%; Score 93; DB 22; Length 39;

DB Best Local Similarity 68.8%; Pred. No. 8.5e-10; Indels 0; Gaps 0;

Matches 22; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

RESULT 30
AAE08381
ID AAE08381 standard; peptide; 39 AA.
DB 4 GTFTSDLSKQLEEAVALRFLFELKNGXSSGA 35

AAE08381;

DT 01-NOV-2001 (first entry)

DE Exendin agonist peptide #28.

XX Exendin agonist; antilipemic; cardiatic; triglyceride; inotropic;
KM diuretic; coronary heart disease; dyslipidaemia.

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 31 /note= "N-Methyl-alanine"

FT Modified-site 36 /note= "N-Methyl-alanine"

FT Modified-site 37 /note= "N-Methyl-alanine"

FT Modified-site 38 /note= "N-Methyl-alanine"

FT Modified-site 39 /note= "N-Methyl-alanine"

FT Modified-site 39 /note= "C-terminal amide"

PN W0200151078-A1.

PD 19-JUL-2001.

PF 09-JAN-2001; 2001WO-US00719.

PR 10-JAN-2000; 2000US-0175365.

PA (AMYL-) AMYLIN PHARM INC.

PI Kolterman OG, Young AA;

XX WPI; 2001-514422/56.

DR WPI; 2001-514422/56.

XX Use of exendin and exendin agonist compounds for modulating

PT triglyceride levels, and treating heart disease and dyslipidemia

XX Example 28; Page -; 161pp; English.

XX The patent discloses a method for modulating plasma or postprandial

CC triglyceride and other lipid levels by administering exendin or an

CC exendin agonist. Exendins have inotropic and diuretic effects. They

CC suppress the secretion of glucagon. Exendin and its agonists have

CC a significant effect on the reduction of blood serum triglyceride

CC concentrations. They are used to treat coronary heart disease and

CC dyslipidaemia, and for modifying postprandial triglyceride levels.

CC Note: The present peptide sequence is an agonist of exendin.

CC Note: The present sequence is not shown in the specification but is

CC derived from SEQ ID NO.3 shown in page 17 of the specification.

XX Sequence 39 AA;

XX Query Match 76.9%; Score 93; DB 22; Length 39;

DB Best Local Similarity 65.6%; Pred. No. 8.5e-10; Indels 0; Gaps 0;

Matches 21; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

4 GTXXXXXSKQEEAVRLXXXXLKNKGXSSGA 35

4 GTFTSDLSKQLEEAVALRFLFELKNGXSSGA 35

Search completed: December 23, 2003, 10:01:24

Job time : 37.5 secs

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OW protein - protein search, using sw model

Run on: December 23, 2003, 09:59:56 ; Search time 13.5 Seconds
(without alignments)
284.944 Million cell updates/sec

Title: US-09-889-331a-47
Perfect score: 121
Sequence: 1 XXXGTXXXXXSKQEEAVRLXXXXLKNCGSSGAXXXXX 40

Scoring table: BL0SUM62
Gapop 10.0, Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database: 1: PIR_76:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	91	75.2	39	1	HMGH32
2	91	75.2	39	1	HMGH4G
3	42	34.7	310	2	D86675
4	42	34.7	546	2	G64803
5	42	34.7	546	2	G85568
6	42	34.7	546	2	G90718
7	42	34.7	546	2	AGS586
8	41	33.9	157	2	G75266
9	41	33.9	357	2	T38405
10	41	33.9	402	2	A75054
11	41	33.9	2044	2	T13704
12	41	33.9	2064	2	T13707
13	40	33.1	127	2	T46374
14	40	33.1	609	2	T46377
15	40	33.1	772	2	T06154
16	39	32.2	208	2	D71137
17	39	32.2	341	2	A40706
18	39	32.2	688	2	E71845
19	39	32.2	688	2	E64671
20	39	32.2	1649	2	C86822
21	38.5	31.8	653	2	T02080
22	38.5	31.8	1702	2	T14050
23	38	31.4	272	2	A42847
24	38	31.4	274	2	G97624
25	38	31.4	300	2	E71023
26	38	31.4	300	2	E75110
27	38	31.4	357	2	JC4703
28	38	31.4	357	2	I49338
29	38	31.4	381	2	A57059

30	38	31.4	419	2	S23018	DNA ligase (ATP) (
31	38	31.4	421	2	C85644	hypothetical prote
32	38	31.4	421	2	A90784	hypothetical prote
33	38	31.4	616	2	T45640	beta-D-glucan exoh
34	38	31.4	726	2	T20183	hypothetical prote
35	38	31.4	816	2	D96344	unknown protein [i
36	38	31.4	1464	2	T13716	barocsa gene prote
37	37.5	31.0	488	2	C85062	probable thiorodox
38	37.5	31.0	608	2	D87912	protein B0205.3 (i
39	37	30.6	157	2	B83897	hypothetical prote
40	37	30.6	189	2	AD2916	transcription regu
41	37	30.6	189	2	G97690	hypothetical prote
42	37	30.6	250	2	A10195	conserved hypothet
43	37	30.6	250	2	A11458	conserved hypothet
44	37	30.6	356	2	H90168	GTP-binding protei
45	37	30.6	430	2	S50604	AST2 protein - yea
46	37	30.6	488	2	S40706	hypothetical prote
47	37	30.6	624	2	T04414	probable glucan 1,
48	37	30.6	628	2	T51283	glucan 1,3-beta-gl
49	37	30.6	850	2	T13352	str-A protein - fr
50	37	30.6	938	2	T05533	hypothetical prote

ALIGNMENTS

RESULT 1
HMGH32
extendin-3 - Mexican beaded lizard
C:Species: Heloderma horridum (Mexican beaded lizard)
C:Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 21-Nov-1997.
C:Accession: A23674
R:Eng, J.; Andrews, P.C.; Kleinman, W.A.; Singh, L.; Raufman, J.P.
J. Biol. Chem. 265, 20259-20262, 1990
A:Title: Purification and structure of extendin-3, a new pancreatic secretagogue isolat.
A:Reference number: A23674; MUID:91056067; PMID:1700785
A:Accession: A23674
A:Molecule type: protein
A:Residues: 1-39 <ENG>
C:Comment: Extendin are venom components that are thought to bind to receptors for vas.
g in secretion of amyase.
C:Superfamily: glucagon
C:Keywords: amidated carboxyl end; duplication; secretagogue; venom
F39/Modified site: amidated carboxyl end (Ser) #status experimental

Query Match 75.2%; Score 91; DB 1; Length 39;
Best Local Similarity 65.6%; Pred. No. 7.8e-10;
Matches 21; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 4 GTYXXXXSKQEEAVRLXXXXLKNCGSSGA 35
DB 4 GTFTSDLSKQEEAVRLFLEMLKNGSPSSGA 35

RESULT 2
HMGH4G
extendin-4 - Gila monster
C:Species: Heloderma suspectum (Gila monster)
C:Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 21-Nov-1997
C:Accession: A42486
R:Eng, J.; Kleinman, W.A.; Singh, L.; Singh, G.; Raufman, J.P.
U. Biol. Chem. 267, 7402-7405, 1992
A:Title: Isolation and characterization of extendin-4, an extendin-3 analogue, from Helo.
A:Reference number: A42486; MUID:92218391; PMID:1313797
A:Accession: A42486
A:Molecule type: protein
A:Residues: 1-39 <ENG>
C:Comment: Extendin-4 does not stimulate amylase secretion by pancreatic acinar cells.
C:Superfamily: glucagon
C:Keywords: amidated carboxyl end; duplication; venom
F39/Modified site: amidated carboxyl end (Ser) #status experimental

Query Match 75.2%; Score 91; DB 1; Length 39;

Best Local Similarity 65.6%; Pred. No. 7.8e-10;
Matches 21; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 4 GTXXXXXSKXXEAVRLXXXXLKNKGXSSGA 35
DB 4 GTFTDSLKQKXEEAVRLFTMLKXNGSPSSGA 35

RESULT 3

DB6675
nevalonate kinase [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C/Species: Lactococcus lactis subsp. lactis
C/Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C/Accession: DB6675
R/Bolotin, A.; Wincker, P.; Manger, S.; Jallion, O.; Marme, K.; Weissenbach, J.; Ehrlich
Genome Res. 11, 731-753, 2001
A/Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp
A/Reference number: AB6625; MUID:21235186; PMID:11337471
A/Accession: DB6675
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-310 <STO>
A/Cross-references: GB:AE005176; PID:912723278; PIDN:AAK04502.1; GSPDB:GN00146
A/Experimental source: strain IL1403
C/Genetics:
A/Gene: yeag

Query Match 34.7%; Score 42; DB 2; Length 310;
Best Local Similarity 33.3%; Pred. No. 6.9;
Matches 7; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 13 OXEEAVRLXXXXLKNKGXSS 33
DB 285 ENKDAIRISQRLKNGAKMT 305

RESULT 4

G64803
phosphoglucumutase (EC 5.4.2.2) - Escherichia coli (strain K-12)
C/Species: Escherichia coli
C/Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C/Accession: G64803; J55076
R/Baltner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A/Title: The complete genome sequence of Escherichia coli K-12.
A/Reference number: A64720; MUID:97426617; PMID:9278503
A/Accession: G64803
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-546 <BIAT>
A/Cross-references: GB:AE000172; GB:U00096; NID:91786896; PIDN:AACT3782.1; PID:91786904;
A/Experimental source: strain K-12, substrain MGL655
R/Liu, M.; Kleckner, N.
J. Bacteriol. 176, 5847-5851, 1994
A/Title: Molecular cloning and characterization of the pgm gene encoding phosphoglucumut
A/Reference number: J55076; MUID:94364967; PMID:8083177
A/Accession: J55076
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-21, 'M', 23-546 <RES>
A/Cross-references: EMBL:U08369; NID:9473887; PIDN:AAA57067.1; PID:9473888
C/Genetics:
A/Gene: pgm
C/Function: conversion of D-glucose 1-phosphate into D-glucose 6-phosphate; participa

C/Superfamily: phosphoglucumutase
C/Keywords: intramolecular transferase; isomerase; phosphoprotein
F/146/Active site: Ser (phosphoserine intermediate) #status predicted
Query Match 34.7%; Score 42; DB 2; Length 546;
Best Local Similarity 52.9%; Pred. No. 13;
Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 12 KOXEEAVRLXXXXLKN 28
DB 529 KOIEKAEIVSEVLKN 545

RESULT 5

G85568
phosphoglucumutase [imported] - Escherichia coli (strain O157:H7, substrain EDL933)
C/Species: Escherichia coli
C/Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 17-May-2002
C/Accession: G85568
R/Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayh
iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; DiMantia, E.; Potamousis, K.; Apodac
Nature 409, 529-533, 2001
A/Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A/Reference number: AB5480; MUID:21074935; PMID:11206551
A/Accession: G85568
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-546 <STO>
A/Cross-references: GB:AE005174; NID:912513593; PIDN:AA65011.1; GSPDB:GN00145; UMGF:Z
A/Experimental source: strain O157:H7, substrain EDL933
C/Genetics:
A/Gene: pgm
C/Superfamily: phosphoglucumutase

Query Match 34.7%; Score 42; DB 2; Length 546;
Best Local Similarity 52.9%; Pred. No. 13;
Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 12 KOXEEAVRLXXXXLKN 28
DB 529 KOIEKAEIVSEVLKN 545

RESULT 6

G90718
phosphoglucumutase [imported] - Escherichia coli (strain O157:H7, substrain RIMD 05099
C/Species: Escherichia coli
C/Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 17-May-2002
C/Accession: G90718
R/Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.
gawara, N.; Yasunaga, T.; Kuhnara, S.; Shiba, T.; Hattoori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A/Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and ge
A/Reference number: AB9629; MUID:21156231; PMID:11258796
A/Accession: G90718
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-546 <HAY>
A/Cross-references: GB:BA000007; PIDN:BA834142.1; PID:913360177; GSPDB:GN00154
A/Experimental source: strain O157:H7, substrain RIMD 0509952
C/Genetics:
A/Gene: Eco719
C/Superfamily: phosphoglucumutase

Query Match 34.7%; Score 42; DB 2; Length 546;
Best Local Similarity 52.9%; Pred. No. 13;
Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 12 KOXEEAVRLXXXXLKN 28
DB 529 KOIEKAEIVSEVLKN 545

RESULT 7

AG0586
phosphoglucumutase [imported] - Salmonella enterica subsp. enterica serovar Typhi (str
C/Species: Salmonella enterica subsp. enterica serovar Typhi
A/Note: this species has also been called Salmonella typhi
C/Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C/Accession: AG0586

R.Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Main, J.; Churcher, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Garra, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A:Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serov
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AC0586
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-546 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD05161.1; PID:G16501934; GSPDB:GN00176
C:Genetics:
A:Gene: STY0736
C:Superfamily: phosphoglucomutase

Query Match 34.7%; Score 42; DB 2; Length 546;
Best Local Similarity 52.9%; Pred. No. 13;
Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 12 KXEEAVRLXXXXLKN 28
DB 529 KQIEKAEIVSEVLKN 545

RESULT 8

G75266
hypothetical protein DR2500 - *Deinococcus radiodurans* (strain R1)

C:Species: *Deinococcus radiodurans*
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000

C:Accession: G75266
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.U.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
Science 286, 1571-1577, 1999

A:Title: Genome sequence of the radioresistant bacterium *Deinococcus radiodurans* R1.
A:Reference number: A75250; MUID:20036896; PMID:10567266

A:Accession: G75266
A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-157 <WH1>

A:Cross-references: GB:AE002079; GB:AE000513; NID:G6460315; PIDN:AAFI2045.1; PID:G646032
A:Experimental source: strain R1

C:Genetics:
A:Gene: DR2500

A:Map position: 1
C:Superfamily: *Deinococcus radiodurans* hypothetical protein DR2500

Query Match 33.9%; Score 41; DB 2; Length 157;
Best Local Similarity 42.1%; Pred. No. 5.1;

Matches 8; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 16 EBAVRLXXXXLKNXGSSG 34
DB 74 DDVQVFRALKNAGIDSG 92

RESULT 9

T38405
hypothetical protein SPAC26A3.17c - fission yeast (*Schizosaccharomyces pombe*)

C:Species: *Schizosaccharomyces pombe*
C>Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 20-Oct-2000

C:Accession: T38405; T39165
R:McLean, U.; Harris, D.; Barrett, B.G.; Rajandream, M.A.; Walsh, S.V.

A:Reference number: 221791
A:Accession: T38405

A:Molecule type: DNA

A:Residues: 77-357 <MC1>
A:Cross-references: EMBL:269240; PIDN:CA93240.1; GSPDB:GN00066; SPDB:SPAC26A3.17c

A:Experimental source: strain 972h; cosmid 26A3
R:McLean, U.; Harris, D.; Wood, V.; Barrett, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, February 1998

A:Reference number: Z21831

A:Accession: T39165

A:Molecule type: DNA

A:Residues: 1-141 <MC2>
A:Cross-references: EMBL:AL021817; PIDN:CAB40198.1; GSPDB:GN00066; SPDB:SPAC8E11.11

A:Experimental source: strain 972h; cosmid 8E11
C:Genetics:
A:Gene: SPAC8E11.07; SPDB:SPAC26A3.17c; SPDB:SPAC8E11.11

Query Match 33.9%; Score 41; DB 2; Length 357;
Best Local Similarity 34.8%; Pred. No. 12;
Matches 8; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 12 KXEEAVRLXXXXLKNXGSSG 34
DB 64 KETEVQAEIVTKWILSNGGVWG 86

RESULT 10

A75054
molybdenum cofactor biosynthesis protein (moa-1) PAB1436 - *Pyrococcus abyssi* (strain

C:Species: *Pyrococcus abyssi*
C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000

C:Accession: A75054
R:anonymous, Genoscope

submitted to the EMBL Data Library, July 1999
A:Description: *Pyrococcus abyssi* genome sequence: insights into archaeal chromosome s

A:Reference number: A75001

A:Accession: A75054

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-402 <KMW>
A:Cross-references: GB:A248287; GB:AL096836; NID:G5458657; PIDN:CAB50326.1; PID:G545

A:Experimental source: strain Oresay
C:Genetics:

A:Gene: PAB1436
C:Superfamily: molybdenum cofactor biosynthesis protein moa-2

Query Match 33.9%; Score 41; DB 2; Length 402;
Best Local Similarity 39.1%; Pred. No. 14;
Matches 9; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 12 KXEEAVRLXXXXLKNXGSSG 34
DB 237 KETIEGVRVADIVISGASGG 259

RESULT 11
T13704
still life protein type 2 - fruit fly (*Drosophila melanogaster*)

C:Species: *Drosophila melanogaster*
C>Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000

C:Accession: T13704
R:Song, M.; Hoshino, M.; Suzuki, E.; Kuroda, S.; Kaibuchi, K.; Nakagoshi, H.; Saigo,

Science 275, 543-547, 1997
A:Title: Still life, a protein in synaptic terminals of *Drosophila* homologous to GDP-

A:Reference number: Z17701; MUID:97153054; PMID:8999801
A:Accession: T13704

A:Status: preliminary; translated from GB/EMBL/DD81

A:Molecule type: mRNA

A:Residues: 1-2044 <SON>
A:Cross-references: EMBL:D6546; NID:G1813375; PIDN:BA13108.1; PID:G1813376

C:Genetics:
A:Cross-references: FlyBase:FBgn0019652

Query Match 33.9%; Score 41; DB 2; Length 2044;
Best Local Similarity 41.7%; Pred. No. 78;
Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 12 KXEEAVRLXXXXLKNXGSSG 35
DB 1761 RQIRRESVRVMSIPMKNGFGSSGS 1784

RESULT 12

T13707
still life protein type 1 - fruit fly (*Drosophila melanogaster*)
C/Species: *Drosophila melanogaster*
C/Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
C/Accession: T13707
R/Sone, M.; Hoshino, M.; Suzuki, E.; Kuroda, S.; Kaibuchi, K.; Nakagoshi, H.; Saigo, K.;
Science 275, 543-547, 1997
A/Title: Still life, a protein in synaptic terminals of *Drosophila* homologous to GDP-GTF
A/Reference number: 217701; MUID:9715054; PMID:8999801
A/Accession: T13707
A/Status: preliminary; translated from GB/EMBL/DBD
A/Molecule type: mRNA
A/Residues: 1-2064 <SON>
A/Cross-references: EMBL:D86547; NID:G123377; PIDN:BA13109.1; PID:91813378
C/Genetics:
A/Cross-references: FlyBase:FBgn0019652

Query Match 33.1%; Score 40; DB 2; Length 2064;
Best Local Similarity 41.7%; Pred. No. 79;
Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

OY 12 KXEEAVRLXXXXLKNGXSSGA 35
DB 1781 RQTRRSVRNMSIMKNGSSGS 1804

RESULT 13

CG9774

transcription regulator phage-related homolog ydcN - *Bacillus subtilis*
C/Species: *Bacillus subtilis*
C/Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000

C/Accession: CG9774
R/Kunst, F.; Ogasawara, N.; Moser, I.; Albertini, A.M.; Alloni, G.; Avevedo, V.; Berter
C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capiano, V.; Carter, N.M.; Cinc
A.; Ehrlich, S.D.; Emerson, P.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997

A/Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallet
A.; Harwood, C.R.; Hensut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
leth, J.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
Koester, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A/Authors: Lauder, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maue
Y., M.; Ogawa, K.; Ogilwa, A.; Oudega, B.; Park, S.H.; Paro, V.; Pohl, T.M.; Portecelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadle, Y.; Sato, T.; Scanlon,
A/Authors: Schleich, S.; Schroeter, R.; Scofield, F.; Sekiguchi, J.; Sekowaka, A.; Serot
akuchi, M.; Tanakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Waters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasunoto, K.; Yata, K.; Yoshida, K.
A/Authors: Yoshikawa, H.F.; Zumbach, E.; Yoshikawa, H.; Danchin, A.
A/Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.
A/Reference number: A69580; MUID:98044033; PMID:9384377

A/Accession: CG9774
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-127 <KUN>
A/Cross-references: GB:299106; GB:AL009126; NID:G2632653; PIDN:CB12289.1; PID:G2632782
A/Experimental source: strain 168
C/Genetics:
A/Cene: ydcN
C/Superfamily: probable transcription repressor yowR

Query Match 33.1%; Score 40; DB 2; Length 127;
Best Local Similarity 47.1%; Pred. No. 63;
Matches 8; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

OY 13 QXEEAVRLXXXXLKNG 29
DB 100 EFDEETARLVKXKNG 116

RESULT 14

T45637
beta-D-glucan exohydrolase-like protein - *Arabidopsis thaliana*

N/Alternate names: protein F1312.60

C/Species: *Arabidopsis thaliana* (mouse-ear cress)

C/Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 21-Jul-2000

C/Accession: T45637
R/Choise, N.; Robert, C.; Brothier, P.; Winkler, P.; Calcolico, L.; Artiguenave, F.;

submitted to the Protein Sequence Database, November 1999

A/Reference number: 223010

A/Accession: T45637

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-609 <CHO>

A/Cross-references: EMBL:AL133292

A/Experimental source: cultivar Columbia; BAC clone F1312

C/Genetics:
A/Map position: 3
A/Introns: 57/1; 125/2; 155/3; 204/2; 285/3; 320/3; 381/3; 449/1
A/Note: F1312.60

C/Superfamily: beta-glucosidase

Query Match 33.1%; Score 40; DB 2; Length 609;
Best Local Similarity 38.5%; Pred. No. 33;
Matches 10; Conservative 2; Mismatches 14; Indels 0; Gaps 0;

OY 4 GTXXXXXSKXEEAVRLXXXXLKNG 29
DB 376 GTVGCXKXREAVRKSIVLLKNG 401

RESULT 15

T06154

hypothetical protein F24J7.162 - *Arabidopsis thaliana*

C/Species: *Arabidopsis thaliana* (mouse-ear cress)

C/Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 22-Oct-1999

C/Accession: T06154

R/Bevan, M.; Vitale, D.; Liguori, R.; Argitrou, A.; De Simone, V.; Bancroft, I.; Mewe

submitted to the Protein Sequence Database, April 1999

A/Reference number: 215493

A/Accession: T06154

A/Molecule type: DNA

A/Residues: 1-772 <BEV>

A/Cross-references: EMBL:AL021768; GSPD:GN00062; ATSP:F24J7.162

A/Experimental source: cultivar Columbia; BAC clone F24J7

C/Genetics:
A/Map position: 4
A/Introns: 4/2; 42/3; 273/2; 303/2; 342/3; 346/1; 463/3; 485/2; 536/3; 548/3; 576/3;

Query Match 33.1%; Score 40; DB 2; Length 772;
Best Local Similarity 37.5%; Pred. No. 43;
Matches 9; Conservative 3; Mismatches 12; Indels 0; Gaps 0;

OY 11 SKXEEAVRLXXXXLKNGXSSG 34
DB 60 SHKXEEAVRLXXXXLKNGXSSG 83

RESULT 16

D71137

probable transcription initiation factor IIB - *Pyrococcus horikoshii*

C/Species: *Pyrococcus horikoshii*

C/Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 21-Jul-2000

C/Accession: D71137

R/Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Hatake, Y.; Hino, Y.; Yamamoto, S.; Se

M.; Ohnuki, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kishida, N.; Og

DNA Res. 5, 55-76, 1998

A/Title: Complete sequence and gene organization of the genome of a hyper-thermophilic

A/Reference number: A71000; MUID:98344137; PMID:9679194

A/Accession: D71137

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-208 <KAW>

A/Cross-references: GB:AP000003; NID:G3236130; PIDN:BAA29958.1; PID:G3257275

A/Experimental source: strain OT3

A:Experimental source: strain Golden Bantam; mesophyll
C:Function:
A:Description: catalyzes the reversible hydration of carbon dioxide
C:Superfamily: Escherichia coli carbonate dehydratase
C:Keywords: carbon-oxygen lyase; hydro-lyase; metalloprotein; zinc

Query Match 31.8%; Score 38.5; DB 2; Length 653;
Best Local Similarity 37.9%; Pred. No. 67;
Matches 11; Conservative 3; Mismatches 6; Indels 9; Gaps 1;

QY 15 EEEAVRLXXXXLKN-----GKXSSG 34
DB 407 EKEAVNVLQNLKSLPLVKEGLAGGTSSG 435

RESULT 22

T14050
protein kinase (EC 2.7.1.37) beta, myotonic dystrophy-associated - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jun-2000
C:Accession: T14050
R:Leung, T.; Chen, X.Q.; Tan, I.; Manser, E.; Lim, L.
Mol. Cell. Biol. 18, 130-140, 1998
A:Title: Myotonic dystrophy kinase-related Cdc42-binding kinase acts as a Cdc42 effector
A:Reference number: 217862; PMID:98078670; PMID:9418861
A:Accession: T14050
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1702 <E17>
A:Cross-references: EMBL:AF021935; NID:G2736152; PID:G2736153; PIDN:AA02942.1
A:Experimental source: brain
C:Genetics:
A:Gene: MRCK-beta
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo
C:Keywords: ATP; phosphotransferase
F:74-342/Domain: protein kinase homology <KIN>
F:1027-1076/Domain: protein kinase C zinc-binding repeat homology <KZN>

Query Match 31.8%; Score 38.5; DB 2; Length 1702;
Best Local Similarity 44.0%; Pred. No. 1.9e+02;
Matches 11; Conservative 1; Mismatches 10; Indels 3; Gaps 1;

QY 11 SKQEEAVRLXXXXLKNKGXSSGA 35
DB 654 SKQERE---LELVKTKQGGRCGPA 675

RESULT 23

AH2847
pyrroline-5-carboxylate reductase [imported] - Agrobacterium tumefaciens (strain C58, Du
C:Species: Agrobacterium tumefaciens
C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C:Accession: AH2847
R:Wood, D.W.; Seubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavlin, T.; Levy, R.; Li, M.; McClell
Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; MUID:2160550; PMID:11743193
A:Accession: AH2847
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-272 <K1R>
A:Cross-references: GB:AE006868; PIDN:AA43198.1; PID:G17740678; GSPDB:GN00186
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: Proc
A:Map position: circular chromosome
C:Superfamily: pyrroline-5-carboxylate reductase

Query Match 31.4%; Score 38; DB 2; Length 272;

Best Local Similarity 39.1%; Pred. No. 33;
Matches 9; Conservative 2; Mismatches 12; Indels 0; Gaps 0;

QY 13 OXEEAVRLXXXXLKNKGXSSGA 35
DB 220 QSPBEAARLRQVITSPGCTTAA 242

RESULT 24

G97624
delta 1-pyrroline-5-carboxylate reductase (AF302126) [imported] - Agrobacterium tumefa
C:Species: Agrobacterium tumefaciens
C>Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
C:Accession: G97624
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Ourullo, B.; Goldma
A.; Liu, F.; Mollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B
Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium t
A:Reference number: A97359; MUID:21608551; PMID:11743194
A:Accession: G97624
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-274 <K1R>
A:Cross-references: GB:AE007869; PIDN:AAK97952.1; PID:G15157356; GSPDB:GN00169
C:Genetics:
A:Gene: AGR_C 4015
A:Map position: circular chromosome
C:Superfamily: pyrroline-5-carboxylate reductase

Query Match 31.4%; Score 38; DB 2; Length 274;
Best Local Similarity 39.1%; Pred. No. 33;
Matches 9; Conservative 2; Mismatches 12; Indels 0; Gaps 0;

QY 13 OXEEAVRLXXXXLKNKGXSSGA 35
DB 222 QSPBEAARLRQVITSPGCTTAA 244

RESULT 25

E71023
probable transcription initiation factor IIB - Pyrococcus horikoshii
C:Species: Pyrococcus horikoshii
C>Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 20-Jun-2000
C:Accession: E71023
R:Kawarayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sek
M.; Ohtoku, Y.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.; Kushida, N.; Oguc
DNA Res. 5, 55-76, 1998
A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic
A:Reference number: A71000; MUID:98344137; PMID:9679194
A:Accession: E71023
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-300 <KAN>
A:Cross-references: GB:AF000006; NID:G3236133; PIDN:BAA30389.1; PID:G3257906
A:Experimental source: strain OT3
A:Note: this accession replaces an interim accession for a sequence replaced by GenBar
C:Genetics:
A:Gene: PH1482
C:Superfamily: transcription initiation factor IIB; transcription initiation factor II
C:Keywords: transcription initiation
F:6-291/Domain: transcription initiation factor IIB homology <TFB>

Query Match 31.4%; Score 38; DB 2; Length 300;
Best Local Similarity 44.4%; Pred. No. 36;
Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 12 KOXEEAVRLXXXXLKN 29
DB 127 KHVEEAAALVREAVRKG 144

RESULT 26

E75110

transcription initiation factor IIB PAB1912 - Pyrococcus abyssi (strain Orsay)
 C/Species: Pyrococcus abyssi
 C/Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
 C/Accession: E75110
 R/Anonymous: Genoscope
 A/Submitted to: EMBL Data Library, July 1999
 A/Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
 A/Reference number: A75001
 A/Accession: E75110
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-300 <RAW>
 A/Cross-references: GB:AU248285; GB:AL096836; NID:95458067; PIDN:CAE49598.1; PID:9545810
 A/Experimental source: strain Orsay
 C/Genetics:
 A/Gene: PAB1912
 C/Superfamily: transcription initiation factor IIB; transcription initiation factor IIB
 C/Keywords: transcription initiation factor IIB homology <TF2>
 F/6-291/Domain: transcription initiation factor IIB homology <TF2>

Query Match 31.4%; Score 38; DB 2; Length 300;
 Best Local Similarity 44.1%; Pred. No. 36;
 Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 12 KOXEEAVRLXXXXLKNG 29
 DB 127 KXEEAARLYREAVRKG 144

RESULT 27
 UC4703
 Basic helix-loop-helix factor 1 - rat
 N/Alternate names: BHLH
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 20-Jun-2000
 C/Accession: J04703
 R/Kawakami, H.; Maruyama, H.; Yasunami, M.; Okubo, H.; Hara, H.; Saiga, T.; Nakanishi, R.
 Biochem. Biophys. Res. Commun. 221, 199-204, 1996
 A/Title: Cloning and expression of a rat brain basic helix-loop-helix factor.
 A/Reference number: J04703; MUID:96220182; PMID:8660336
 A/Accession: J04703
 A/Molecule type: mRNA
 A/Residues: 1-357 <RAW>
 A/Cross-references: DDBJ:D82075; NID:G1369912; PIDN:BA11536.1; PID:G1369913
 C/Comment: This factor works as transcriptional factor to regulate myogenesis and neuroge
 C/Genetics:
 A/Gene: BHLH
 F/58-78/Region: helix-loop-helix structure predicted
 F/102-157/Region: helix-loop-helix structure predicted

Query Match 31.4%; Score 38; DB 2; Length 357;
 Best Local Similarity 42.1%; Pred. No. 44;
 Matches 8; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 12 KOXEEAVRLXXXXLKNG 30
 DB 39 KEDELAMNNAEDSLRNG 57

RESULT 28
 I49338
 neurogenic differentiation factor - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 02-Jul-1996 #sequence_revision 16-Aug-1996 #text_change 05-Nov-1999
 C/Accession: I49338; I49345
 R/Lee, J.E.; Hollenberg, S.M.; Snider, L.; Turner, D.L.; Lipnick, N.; Weintraub, H.
 Science 268, 836-844, 1995
 A/Title: Conversion of Xenopus ectoderm into neurons by NeuroD, a basic helix-loop-helix
 A/Reference number: A56481; MUID:95273957; PMID:7754368
 A/Accession: I49338
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 73-357 <RE2>

A/Cross-references: EMBL:U28068; NID:9854738; PIDN:AAC52203.1; PID:9854739
 A/Accession: I49345
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-121 <RE3>
 A/Cross-references: EMBL:U28888; NID:9854742; PIDN:AAC52204.1; PID:9854743
 C/Genetics:
 A/Gene: neuroD

Query Match 31.4%; Score 38; DB 2; Length 357;
 Best Local Similarity 42.1%; Pred. No. 44;
 Matches 8; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 12 KOXEEAVRLXXXXLKNG 30
 DB 39 KEDELAMNNAEDSLRNG 57

RESULT 29
 A57059
 beta-cell E-box transcription activator 2 - hamster (fragment)
 C/Species: Cricetinae gen. sp. (hamster)
 C/Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 08-Oct-1999
 C/Accession: A57059
 R/Naya, F.J.; Stellrecht, C.M.M.; Tsai, M.J.
 Genes Dev. 9, 1009-1019, 1995
 A/Title: Tissue-specific regulation of the insulin gene by a novel basic helix-loop-he
 A/Reference number: A57059; MUID:9523222; PMID:7774807
 A/Accession: A57059
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-381 <NAV>
 A/Cross-references: GB:U24679; NID:9777418; PIDN:AAA86518.1; PID:9777419

Query Match 31.4%; Score 38; DB 2; Length 381;
 Best Local Similarity 42.1%; Pred. No. 47;
 Matches 8; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 12 KOXEEAVRLXXXXLKNG 30
 DB 65 KEDELAMNNAEDSLRNG 83

RESULT 30
 S23018
 DNA ligase (ATP) (EC 6.5.1.1) - African swine fever virus
 C/Species: African swine fever virus, ASFV
 C/Date: 03-Mar-1994 #sequence_revision 19-Oct-1995 #text_change 16-Jul-1999
 C/Accession: S23018
 R/Hammond, J.M.; Kerr, S.M.; Smith, G.L.; Dixon, L.K.
 Nucleic Acids Res. 20, 2667-2671, 1992
 A/Title: An African swine fever virus gene with homology to DNA ligases.
 A/Reference number: S23018; MUID:92310959; PMID:1614852
 A/Accession: S23018
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-419 <HAM>
 A/Cross-references: EMBL:X65192; NID:958645; PIDN:CAA46310.1; PID:958646
 C/Superfamily: African swine fever virus DNA ligase
 C/Keywords: ATP; DNA recombination; DNA repair; ligase; phosphoprotein
 F/151/Active site: Lys (covalent AMP-binding) #status predicted

Query Match 31.4%; Score 38; DB 2; Length 419;
 Best Local Similarity 42.1%; Pred. No. 52;
 Matches 8; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 11 SKXEEAVRLXXXXLKNG 29
 DB 271 SYKNDEALRLKQPIKNG 289

Search completed: December 23, 2003, 10:02:38
 Job time: 15.5 secs

Mon Dec 29 06:32:06 2003

us-09-889-331a-47.rpt

CURRENT FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 189
SOFTWARE: PatentIn Ver. 2.1 and Microsoft Word
SEQ ID NO 99
LENGTH: 37
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: artificial sequence with specific variable residues
NAME/KEY: VARIANT
LOCATION: (31)
OTHER INFORMATION: Xaa is homoproline
NAME/KEY: VARIANT
LOCATION: (36)..(37)
OTHER INFORMATION: Xaa is homoproline
NAME/KEY: MOD_RES
LOCATION: (37)
OTHER INFORMATION: AMIDATION, Position 37 is homoproline-NH2
US-09-323-867A-99

Query Match 76.9%; Score 93; DB 4; Length 37;
Best Local Similarity 68.8%; Pred. No. 4.6e-10;
Matches 22; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 4 GTXXXXXSKQEEAVRLXXXXLKNKGXSSGA 35
DB 4 GTFTSDASKQEEAVRLFTFLKNGXSSGA 35

RESULT 3
US-09-323-867A-183
Sequence 183, Application US/09323867A
Patent No. 6506724
GENERAL INFORMATION:
APPLICANT: Amylin Pharmaceuticals, Inc.
APPLICANT: Young, Andrew et al.
TITLE OF INVENTION: USE OF EXTENDING AND AGONISTS THEREOF FOR THE TREATMENT
TITLE OF INVENTION: OF GESTATIONAL DIABETES MELLITUS
FILE REFERENCE: 030639.0032.U1L2 (243/131US)
CURRENT APPLICATION NUMBER: US/09/323,867A
CURRENT FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 189
SOFTWARE: PatentIn Ver. 2.1 and Microsoft Word
SEQ ID NO 183
LENGTH: 37
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: artificial sequence with specific variable residues
NAME/KEY: VARIANT
LOCATION: (31)
OTHER INFORMATION: Xaa is N-methylalanine
NAME/KEY: VARIANT
LOCATION: (36)..(37)
OTHER INFORMATION: Xaa is N-methylalanine
NAME/KEY: MOD_RES
LOCATION: (37)
OTHER INFORMATION: AMIDATION, Position 37 is N-methylalanine-NH2
US-09-323-867A-183

Query Match 76.9%; Score 93; DB 4; Length 37;
Best Local Similarity 68.8%; Pred. No. 4.6e-10;
Matches 22; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 4 GTXXXXXSKQEEAVRLXXXXLKNKGXSSGA 35
DB 4 GTFTSALSQKEEAVRLFTFLKNGXSSGA 35

RESULT 4
US-09-323-867A-35
Sequence 35, Application US/09323867A
Patent No. 6506724

GENERAL INFORMATION:
APPLICANT: Amylin Pharmaceuticals, Inc.
APPLICANT: Young, Andrew et al.
TITLE OF INVENTION: USE OF EXTENDING AND AGONISTS THEREOF FOR THE TREATMENT
TITLE OF INVENTION: OF GESTATIONAL DIABETES MELLITUS
FILE REFERENCE: 030639.0032.U1L2 (243/131US)
CURRENT APPLICATION NUMBER: US/09/323,867A
CURRENT FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 189
SOFTWARE: PatentIn Ver. 2.1 and Microsoft Word
SEQ ID NO 35
LENGTH: 39
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: artificial sequence with specific variable residues
NAME/KEY: VARIANT
LOCATION: (31)
OTHER INFORMATION: Xaa at position 31 is thioproline
NAME/KEY: VARIANT
LOCATION: (36)..(38)
OTHER INFORMATION: Xaa at positions 36, 37, and 38 is thioproline
NAME/KEY: MOD_RES
LOCATION: (39)
OTHER INFORMATION: AMIDATION, Position 39 is Ser-NH2
US-09-323-867A-35

Query Match 76.9%; Score 93; DB 4; Length 39;
Best Local Similarity 68.8%; Pred. No. 4.8e-10;
Matches 22; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 4 GTXXXXXSKQEEAVRLXXXXLKNKGXSSGA 35
DB 4 GTFTSDLSKQEEAVRLFTFLKNGXSSGA 35

RESULT 5
US-09-323-867A-36
Sequence 36, Application US/09323867A
Patent No. 6506724
GENERAL INFORMATION:
APPLICANT: Amylin Pharmaceuticals, Inc.
APPLICANT: Young, Andrew et al.
TITLE OF INVENTION: USE OF EXTENDING AND AGONISTS THEREOF FOR THE TREATMENT
TITLE OF INVENTION: OF GESTATIONAL DIABETES MELLITUS
FILE REFERENCE: 030639.0032.U1L2 (243/131US)
CURRENT APPLICATION NUMBER: US/09/323,867A
CURRENT FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 189
SOFTWARE: PatentIn Ver. 2.1 and Microsoft Word
SEQ ID NO 36
LENGTH: 39
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: artificial sequence with specific variable residues
NAME/KEY: VARIANT
LOCATION: (31)
OTHER INFORMATION: Xaa at position 31 is homoproline
NAME/KEY: VARIANT
LOCATION: (36)..(38)
OTHER INFORMATION: Xaa at positions 36, 37, and 38 is homoproline
NAME/KEY: MOD_RES
LOCATION: (39)
OTHER INFORMATION: AMIDATION, Position 39 is Ser-NH2
US-09-323-867A-36

Query Match 76.9%; Score 93; DB 4; Length 39;
Best Local Similarity 68.8%; Pred. No. 4.8e-10;
Matches 22; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 4 GTXXXXXSKQEEAVRLXXXXLKNKGXSSGA 35
DB 4 GTFTSALSQKEEAVRLFTFLKNGXSSGA 35

Db 4 GTFTSDLSKQLEBEAVRLFIETLKNKGXSSGA 35

RESULT 6
US-09-323-867A-39
Sequence 39, Application US/09323867A
Patent No. 6506724
GENERAL INFORMATION:
APPLICANT: Amylin Pharmaceuticals, Inc.
APPLICANT: Young, Andrew et al.
TITLE OF INVENTION: USE OF EXTENDING AND AGONISTS THEREOF FOR THE TREATMENT
FILE REFERENCE: 030639.0032.UTL2 (243/131US)
CURRENT FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 189
SOFTWARE: PatentIn Ver. 2.1 and Microsoft Word
SEQ ID NO 39
LENGTH: 39
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: artificial sequence with specific variable residues
NAME/KEY: VARIANT
LOCATION: (31)
OTHER INFORMATION: Xaa at position 31 is N-methylalanine
NAME/KEY: VARIANT
LOCATION: (36)..
OTHER INFORMATION: Xaa at positions 36, 37, and 38 is N-methylalanine
NAME/KEY: MOD RES
LOCATION: (39)
OTHER INFORMATION: AMIDATION, Position 39 is Ser-NH2
US-09-323-867A-39

Query Match 76.9%; Score 93; DB 4; Length 39;
Best Local Similarity 68.8%; Pred. No. 4.8e-10;
Matches 22; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 4 GTXXXXXSKQXEEAVRLXXXXLKNKGXSSGA 35
Db 4 GTFTSDLSKQLEBEAVRLFIETLKNKGXSSGA 35

RESULT 7
US-09-323-867A-69
Sequence 69, Application US/09323867A
Patent No. 6506724
GENERAL INFORMATION:
APPLICANT: Amylin Pharmaceuticals, Inc.
APPLICANT: Young, Andrew et al.
TITLE OF INVENTION: USE OF EXTENDING AND AGONISTS THEREOF FOR THE TREATMENT
FILE REFERENCE: 030639.0032.UTL2 (243/131US)
CURRENT FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 189
SOFTWARE: PatentIn Ver. 2.1 and Microsoft Word
SEQ ID NO 69
LENGTH: 35
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: artificial sequence with specific variable residues
NAME/KEY: MOD RES
LOCATION: (35)
OTHER INFORMATION: AMIDATION, Position 35 is Ala-NH2
US-09-323-867A-69

Query Match 76.0%; Score 92; DB 4; Length 35;
Best Local Similarity 65.6%; Pred. No. 6.5e-10;
Matches 21; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 4 GTXXXXXSKQXEEAVRLXXXXLKNKGXSSGA 35

Db 4 GTFTSDLSKQLEBEAVRLFIETLKNKGXSSGA 35

RESULT 8
US-09-323-867A-173
Sequence 173, Application US/09323867A
Patent No. 6506724
GENERAL INFORMATION:
APPLICANT: Amylin Pharmaceuticals, Inc.
APPLICANT: Young, Andrew et al.
TITLE OF INVENTION: USE OF EXTENDING AND AGONISTS THEREOF FOR THE TREATMENT
FILE REFERENCE: 030639.0032.UTL2 (243/131US)
CURRENT FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 189
SOFTWARE: PatentIn Ver. 2.1 and Microsoft Word
SEQ ID NO 173
LENGTH: 35
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: artificial sequence with specific variable residues
NAME/KEY: MOD RES
LOCATION: (35)
OTHER INFORMATION: AMIDATION, Position 35 is Ala-NH2
US-09-323-867A-173

Query Match 76.0%; Score 92; DB 4; Length 35;
Best Local Similarity 65.6%; Pred. No. 6.5e-10;
Matches 21; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 4 GTXXXXXSKQXEEAVRLXXXXLKNKGXSSGA 35
Db 4 GTFTSDLSKQLEBEAVRLFIETLKNKGXSSGA 35

RESULT 9
US-09-323-867A-67
Sequence 67, Application US/09323867A
Patent No. 6506724
GENERAL INFORMATION:
APPLICANT: Amylin Pharmaceuticals, Inc.
APPLICANT: Young, Andrew et al.
TITLE OF INVENTION: USE OF EXTENDING AND AGONISTS THEREOF FOR THE TREATMENT
FILE REFERENCE: 030639.0032.UTL2 (243/131US)
CURRENT FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 189
SOFTWARE: PatentIn Ver. 2.1 and Microsoft Word
SEQ ID NO 67
LENGTH: 36
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: artificial sequence with specific variable residues
NAME/KEY: MOD RES
LOCATION: (36)
OTHER INFORMATION: AMIDATION, Position 36 is Pro-NH2
US-09-323-867A-67

Query Match 76.0%; Score 92; DB 4; Length 36;
Best Local Similarity 65.6%; Pred. No. 6.7e-10;
Matches 21; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 4 GTXXXXXSKQXEEAVRLXXXXLKNKGXSSGA 35
Db 4 GTFTSDLSKQLEBEAVRLFIETLKNKGXSSGA 35

RESULT 10

US-09-323-867A-86

Sequence 86, Application US/09323867A
Patent No. 6506724
GENERAL INFORMATION:
APPLICANT: Amylin Pharmaceuticals, Inc.
TITLE OF INVENTION: USE OF EXTENDING AND AGONISTS THEREOF FOR THE TREATMENT
FILE REFERENCE: 030639.0032.UTL2 (243/131US)
CURRENT APPLICATION NUMBER: US/09/323,867A
CURRENT FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 189
SOFTWARE: Patentin Ver. 2.1 and Microsoft Word
SEQ ID NO 86
LENGTH: 36
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: VARIANT
LOCATION: (31)
OTHER INFORMATION: Xaa is homoproline
NAME/KEY: VARIANT
LOCATION: (36)
OTHER INFORMATION: Xaa is homoproline
NAME/KEY: MOD RES
LOCATION: (36)
OTHER INFORMATION: AMIDATION, Position 36 is homoproline-NH2
US-09-323-867A-86

Query Match 76.0%; Score 92; DB 4; Length 36;
Best Local Similarity 68.8%; Pred. No. 6.7e-10;
Matches 22; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 4 GTXXXXXSKQEEAVRLXXXXLKNKGXSSGA 35
DB 4 GTFTSLSKQEEAVRLFTFLKNGGSSGA 35

RESULT 11

US-09-323-867A-170
Sequence 170, Application US/09323867A
Patent No. 6506724
GENERAL INFORMATION:
APPLICANT: Amylin Pharmaceuticals, Inc.
TITLE OF INVENTION: USE OF EXTENDING AND AGONISTS THEREOF FOR THE TREATMENT
FILE REFERENCE: 030639.0032.UTL2 (243/131US)
CURRENT APPLICATION NUMBER: US/09/323,867A
CURRENT FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 189
SOFTWARE: Patentin Ver. 2.1 and Microsoft Word
SEQ ID NO 170
LENGTH: 36
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: MOD RES
LOCATION: (36)
OTHER INFORMATION: AMIDATION, Position 36 is Pro-NH2
US-09-323-867A-170

Query Match 76.0%; Score 92; DB 4; Length 36;
Best Local Similarity 65.6%; Pred. No. 6.7e-10;
Matches 21; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 4 GTXXXXXSKQEEAVRLXXXXLKNKGXSSGA 35
DB 4 GTFTSLSKQEEAVRLFTFLKNGGSSGA 35

RESULT 12

US-09-323-867A-184
Sequence 184, Application US/09323867A
Patent No. 6506724
GENERAL INFORMATION:
APPLICANT: Amylin Pharmaceuticals, Inc.
TITLE OF INVENTION: USE OF EXTENDING AND AGONISTS THEREOF FOR THE TREATMENT
FILE REFERENCE: 030639.0032.UTL2 (243/131US)
CURRENT APPLICATION NUMBER: US/09/323,867A
CURRENT FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 189
SOFTWARE: Patentin Ver. 2.1 and Microsoft Word
SEQ ID NO 184
LENGTH: 36
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: VARIANT
LOCATION: (31)
OTHER INFORMATION: Xaa is homoproline
NAME/KEY: VARIANT
LOCATION: (36)
OTHER INFORMATION: Xaa is homoproline
NAME/KEY: MOD RES
LOCATION: (36)
OTHER INFORMATION: AMIDATION, Position 36 is homoproline-NH2
US-09-323-867A-184

Query Match 76.0%; Score 92; DB 4; Length 36;
Best Local Similarity 68.8%; Pred. No. 6.7e-10;
Matches 22; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 4 GTXXXXXSKQEEAVRLXXXXLKNKGXSSGA 35
DB 4 GTFTSLSKQEEAVRLFTFLKNGGSSGA 35

RESULT 13

US-09-323-867A-65
Sequence 65, Application US/09323867A
Patent No. 6506724
GENERAL INFORMATION:
APPLICANT: Amylin Pharmaceuticals, Inc.
TITLE OF INVENTION: USE OF EXTENDING AND AGONISTS THEREOF FOR THE TREATMENT
FILE REFERENCE: 030639.0032.UTL2 (243/131US)
CURRENT APPLICATION NUMBER: US/09/323,867A
CURRENT FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 189
SOFTWARE: Patentin Ver. 2.1 and Microsoft Word
SEQ ID NO 65
LENGTH: 37
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: MOD RES
LOCATION: (37)
OTHER INFORMATION: AMIDATION, Position 37 is Pro-NH2
US-09-323-867A-65

Query Match 76.0%; Score 92; DB 4; Length 37;
Best Local Similarity 65.6%; Pred. No. 6.9e-10;
Matches 21; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 4 GTXXXXXSKQEEAVRLXXXXLKNKGXSSGA 35
DB 4 GTFTSLSKQEEAVRLFTFLKNGGSSGA 35

RESULT 14
US-09-323-867A-83
; Sequence 83, Application US/09323867A
; Patent No. 6506724
; GENERAL INFORMATION:
; APPLICANT: Amylin Pharmaceuticals, Inc.
; APPLICANT: Young, Andrew et al.
; TITLE OF INVENTION: USE OF EXTENDING AND AGONISTS THEREOF FOR THE TREATMENT
; TITLE OF INVENTION: OF GESTATIONAL DIABETES MELLITUS
; FILE REFERENCE: 030639.0032.UTL2 (243/131US)
; CURRENT APPLICATION NUMBER: US/09/323,867A
; CURRENT FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 189
; SOFTWARE: Patentin Ver. 2.1 and Microsoft Word
; SEQ ID NO 83
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: artificial sequence with specific variable residues
; NAME/KEY: VARIANT
; LOCATION: (31)
; OTHER INFORMATION: Xaa is N-methylalanine
; NAME/KEY: MOD RES
; LOCATION: (37)
; OTHER INFORMATION: AMIDATION, Position 37 is Pro-NH2
US-09-323-867A-83

Query Match 76.0%; Score 92; DB 4; Length 37;
Best Local Similarity 68.8%; Pred. No. 6.9e-10;
Matches 22; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 4 GTXXXXXSKQEEAVRLXXXXLKNCGXSSGA 35
Db 4 GTFTSDLSKQMEBEAVRLFIEWLKNGXSSGA 35

RESULT 15
US-09-323-867A-84
; Sequence 84, Application US/09323867A
; Patent No. 6506724
; GENERAL INFORMATION:
; APPLICANT: Amylin Pharmaceuticals, Inc.
; APPLICANT: Young, Andrew et al.
; TITLE OF INVENTION: USE OF EXTENDING AND AGONISTS THEREOF FOR THE TREATMENT
; TITLE OF INVENTION: OF GESTATIONAL DIABETES MELLITUS
; FILE REFERENCE: 030639.0032.UTL2 (243/131US)
; CURRENT APPLICATION NUMBER: US/09/323,867A
; CURRENT FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 189
; SOFTWARE: Patentin Ver. 2.1 and Microsoft Word
; SEQ ID NO 84
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: artificial sequence with specific variable residues
; NAME/KEY: VARIANT
; LOCATION: (31)
; OTHER INFORMATION: Xaa is N-methylalanine
; NAME/KEY: MOD RES
; LOCATION: (37)
; OTHER INFORMATION: AMIDATION, Position 37 is N-methylalanine-NH2
US-09-323-867A-84

Query Match 76.0%; Score 92; DB 4; Length 37;
Best Local Similarity 68.8%; Pred. No. 6.9e-10;
Matches 22; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 4 GTXXXXXSKQEEAVRLXXXXLKNCGXSSGA 35
Db 4 GTFTSDLSKQMEBEAVRLFIEWLKNGXSSGA 35

RESULT 16
US-09-323-867A-85
; Sequence 85, Application US/09323867A
; Patent No. 6506724
; GENERAL INFORMATION:
; APPLICANT: Amylin Pharmaceuticals, Inc.
; APPLICANT: Young, Andrew et al.
; TITLE OF INVENTION: USE OF EXTENDING AND AGONISTS THEREOF FOR THE TREATMENT
; TITLE OF INVENTION: OF GESTATIONAL DIABETES MELLITUS
; FILE REFERENCE: 030639.0032.UTL2 (243/131US)
; CURRENT APPLICATION NUMBER: US/09/323,867A
; CURRENT FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 189
; SOFTWARE: Patentin Ver. 2.1 and Microsoft Word
; SEQ ID NO 85
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: artificial sequence with specific variable residues
; NAME/KEY: VARIANT
; LOCATION: (31)
; OTHER INFORMATION: Xaa is homoproline
; NAME/KEY: MOD RES
; LOCATION: (37)
; OTHER INFORMATION: AMIDATION, Position 37 is homoproline-NH2
US-09-323-867A-85

Query Match 76.0%; Score 92; DB 4; Length 37;
Best Local Similarity 68.8%; Pred. No. 6.9e-10;
Matches 22; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 4 GTXXXXXSKQEEAVRLXXXXLKNCGXSSGA 35
Db 4 GTFTSDLSKQMEBEAVRLFIEWLKNGXSSGA 35

RESULT 17
US-09-323-867A-63
; Sequence 63, Application US/09323867A
; Patent No. 6506724
; GENERAL INFORMATION:
; APPLICANT: Amylin Pharmaceuticals, Inc.
; APPLICANT: Young, Andrew et al.
; TITLE OF INVENTION: USE OF EXTENDING AND AGONISTS THEREOF FOR THE TREATMENT
; TITLE OF INVENTION: OF GESTATIONAL DIABETES MELLITUS
; FILE REFERENCE: 030639.0032.UTL2 (243/131US)
; CURRENT APPLICATION NUMBER: US/09/323,867A
; CURRENT FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 189
; SOFTWARE: Patentin Ver. 2.1 and Microsoft Word
; SEQ ID NO 63
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: artificial sequence with specific variable residues
; NAME/KEY: MOD RES
; LOCATION: (38)
; OTHER INFORMATION: AMIDATION, Position 38 is Pro-NH2
US-09-323-867A-63

Query Match 76.0%; Score 92; DB 4; Length 38;
Best Local Similarity 65.6%; Pred. No. 7.1e-10;
Matches 21; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 4 GTXXXXXSKQEEAVRLXXXXLKNKGXSSGA 35
 DB 4 GTFTSLSKQEEAVRLFIEFLKNKGXSSGA 35

RESULT 18
 US-09-323-867A-81
 Sequence 81, Application US/09323867A
 Patent No. 6506724
 GENERAL INFORMATION:
 APPLICANT: Amylin Pharmaceuticals, Inc.
 APPLICANT: Young, Andrew et al.
 TITLE OF INVENTION: USE OF EXTENDING AND AGONISTS THEREOF FOR THE TREATMENT
 TITLE OF INVENTION: OF GESTATIONAL DIABETES MELLITUS
 FILE REFERENCE: 030639.0032.UTL2 (243/131US)
 CURRENT APPLICATION NUMBER: US/09/323,867A
 CURRENT FILING DATE: 1999-06-01
 NUMBER OF SEQ ID NOS: 189
 SOFTWARE: Patentin Ver. 2.1 and Microsoft Word
 SEQ ID NO 81
 LENGTH: 38
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: artificial sequence with specific variable residues
 NAME/KEY: VARIANT
 LOCATION: (31)
 OTHER INFORMATION: Xaa is thioproline
 NAME/KEY: VARIANT
 LOCATION: (36) (38)
 OTHER INFORMATION: Xaa is thioproline
 NAME/KEY: MOD_RES
 LOCATION: (38)
 OTHER INFORMATION: AMIDATION, Position 38 is thioproline-NH2
 US-09-323-867A-81

Query Match 76.0%; Score 92; DB 4; Length 38;
 Best Local Similarity 68.8%; Pred. No. 7.1e-10;
 Matches 22; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 4 GTXXXXXSKQEEAVRLXXXXLKNKGXSSGA 35
 DB 4 GTFTSLSKQEEAVRLFIEFLKNKGXSSGA 35

RESULT 19
 US-09-323-867A-168
 Sequence 168, Application US/09323867A
 Patent No. 6506724
 GENERAL INFORMATION:
 APPLICANT: Amylin Pharmaceuticals, Inc.
 APPLICANT: Young, Andrew et al.
 TITLE OF INVENTION: USE OF EXTENDING AND AGONISTS THEREOF FOR THE TREATMENT
 TITLE OF INVENTION: OF GESTATIONAL DIABETES MELLITUS
 FILE REFERENCE: 030639.0032.UTL2 (243/131US)
 CURRENT APPLICATION NUMBER: US/09/323,867A
 CURRENT FILING DATE: 1999-06-01
 NUMBER OF SEQ ID NOS: 189
 SOFTWARE: Patentin Ver. 2.1 and Microsoft Word
 SEQ ID NO 168
 LENGTH: 38
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: artificial sequence with specific variable residues
 NAME/KEY: MOD_RES
 LOCATION: (38)
 OTHER INFORMATION: AMIDATION, Position 38 is Pro-NH2
 US-09-323-867A-168

Query Match 76.0%; Score 92; DB 4; Length 38;
 Best Local Similarity 65.6%; Pred. No. 7.1e-10;

Matches 21; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
 QY 4 GTXXXXXSKQEEAVRLXXXXLKNKGXSSGA 35
 DB 4 GTFTSLSKQEEAVRLFIEFLKNKGXSSGA 35

RESULT 20
 US-09-323-867A-181
 Sequence 181, Application US/09323867A
 Patent No. 6506724
 GENERAL INFORMATION:
 APPLICANT: Amylin Pharmaceuticals, Inc.
 APPLICANT: Young, Andrew et al.
 TITLE OF INVENTION: USE OF EXTENDING AND AGONISTS THEREOF FOR THE TREATMENT
 TITLE OF INVENTION: OF GESTATIONAL DIABETES MELLITUS
 FILE REFERENCE: 030639.0032.UTL2 (243/131US)
 CURRENT APPLICATION NUMBER: US/09/323,867A
 CURRENT FILING DATE: 1999-06-01
 NUMBER OF SEQ ID NOS: 189
 SOFTWARE: Patentin Ver. 2.1 and Microsoft Word
 SEQ ID NO 181
 LENGTH: 38
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: artificial sequence with specific variable residues
 NAME/KEY: VARIANT
 LOCATION: (31)
 OTHER INFORMATION: Xaa is thioproline
 NAME/KEY: VARIANT
 LOCATION: (36) (38)
 OTHER INFORMATION: Xaa is thioproline
 NAME/KEY: MOD_RES
 LOCATION: (38)
 OTHER INFORMATION: AMIDATION, Position 38 is thioproline-NH2
 US-09-323-867A-181

Query Match 76.0%; Score 92; DB 4; Length 38;
 Best Local Similarity 68.8%; Pred. No. 7.1e-10;
 Matches 22; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 4 GTXXXXXSKQEEAVRLXXXXLKNKGXSSGA 35
 DB 4 GTFTSLSKQEEAVRLFIEFLKNKGXSSGA 35

RESULT 21
 US-09-323-867A-9
 Sequence 9, Application US/09323867A
 Patent No. 6506724
 GENERAL INFORMATION:
 APPLICANT: Amylin Pharmaceuticals, Inc.
 APPLICANT: Young, Andrew et al.
 TITLE OF INVENTION: USE OF EXTENDING AND AGONISTS THEREOF FOR THE TREATMENT
 TITLE OF INVENTION: OF GESTATIONAL DIABETES MELLITUS
 FILE REFERENCE: 030639.0032.UTL2 (243/131US)
 CURRENT APPLICATION NUMBER: US/09/323,867A
 CURRENT FILING DATE: 1999-06-01
 NUMBER OF SEQ ID NOS: 189
 SOFTWARE: Patentin Ver. 2.1 and Microsoft Word
 SEQ ID NO 9
 LENGTH: 39
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: artificial sequence with specific variable residues
 NAME/KEY: MOD_RES
 LOCATION: (39)
 OTHER INFORMATION: AMIDATION, Position 39 is Ser-NH2
 US-09-323-867A-9

Query Match 76.0%; Score 92; DB 4; Length 39;

Best Local Similarity 65.6%; Pred. No. 7.3e-10;
Matches 21; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 4 GTXXXXXSKQXEEAVRLXXXXLKNKGXSSGA 35
DB 4 GTFTSDLSKQXEEAVRLFIETFLKNGGPSSGA 35

RESULT 22
US-09-323-867A-11
Sequence 11, Application US/09323867A
Patent No. 6506724
GENERAL INFORMATION:
APPLICANT: Amylin Pharmaceuticals, Inc.
APPLICANT: Young, Andrew et al.
TITLE OF INVENTION: USE OF EXTENDING AND AGONISTS THEREOF FOR THE TREATMENT
TITLE OF INVENTION: OF GESTATIONAL DIABETES MELLITUS
FILE REFERENCE: 030639.0032.UTL2 (243/131US)
CURRENT APPLICATION NUMBER: US/09/323.867A
CURRENT FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 189
SOFTWARE: PatentIn Ver. 2.1 and Microsoft Word
SEQ ID NO 11
LENGTH: 39
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: artificial sequence with specific variable residues
NAME/KEY: MOD.RES
LOCATION: (39)
OTHER INFORMATION: AMIDATION, Position 39 is Ser-NH2
US-09-323-867A-11

Query Match 76.0%; Score 92; DB 4; Length 39;
Best Local Similarity 65.6%; Pred. No. 7.3e-10;
Matches 21; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 4 GTXXXXXSKQXEEAVRLXXXXLKNKGXSSGA 35
DB 4 GTFTSDLSKQXEEAVRLFIETFLKNGGPSSGA 35

RESULT 23
US-09-323-867A-21
Sequence 21, Application US/09323867A
Patent No. 6506724
GENERAL INFORMATION:
APPLICANT: Amylin Pharmaceuticals, Inc.
APPLICANT: Young, Andrew et al.
TITLE OF INVENTION: USE OF EXTENDING AND AGONISTS THEREOF FOR THE TREATMENT
TITLE OF INVENTION: OF GESTATIONAL DIABETES MELLITUS
FILE REFERENCE: 030639.0032.UTL2 (243/131US)
CURRENT APPLICATION NUMBER: US/09/323.867A
CURRENT FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 189
SOFTWARE: PatentIn Ver. 2.1 and Microsoft Word
SEQ ID NO 21
LENGTH: 39
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: artificial sequence with specific variable residues
NAME/KEY: MOD.RES
LOCATION: (39)
OTHER INFORMATION: AMIDATION, Position 39 is Ser-NH2
NAME/KEY: VARIANT
LOCATION: (10)
OTHER INFORMATION: Xaa is penylglycine
US-09-323-867A-21

Query Match 76.0%; Score 92; DB 4; Length 39;
Best Local Similarity 68.8%; Pred. No. 7.3e-10;
Matches 22; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 4 GTXXXXXSKQXEEAVRLXXXXLKNKGXSSGA 35
DB 4 GTFTSDLSKQXEEAVRLFIETFLKNGGPSSGA 35

RESULT 24
US-09-323-867A-23
Sequence 23, Application US/09323867A
Patent No. 6506724
GENERAL INFORMATION:
APPLICANT: Amylin Pharmaceuticals, Inc.
APPLICANT: Young, Andrew et al.
TITLE OF INVENTION: USE OF EXTENDING AND AGONISTS THEREOF FOR THE TREATMENT
TITLE OF INVENTION: OF GESTATIONAL DIABETES MELLITUS
FILE REFERENCE: 030639.0032.UTL2 (243/131US)
CURRENT APPLICATION NUMBER: US/09/323.867A
CURRENT FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 189
SOFTWARE: PatentIn Ver. 2.1 and Microsoft Word
SEQ ID NO 23
LENGTH: 39
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: artificial sequence with specific variable residues
NAME/KEY: MOD.RES
LOCATION: (39)
OTHER INFORMATION: AMIDATION, Position 39 is Ser-NH2
NAME/KEY: VARIANT
LOCATION: (14)
OTHER INFORMATION: Xaa is penylglycine
US-09-323-867A-23

Query Match 76.0%; Score 92; DB 4; Length 39;
Best Local Similarity 68.8%; Pred. No. 7.3e-10;
Matches 22; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 4 GTXXXXXSKQXEEAVRLXXXXLKNKGXSSGA 35
DB 4 GTFTSDLSKQXEEAVRLFIETFLKNGGPSSGA 35

RESULT 25
US-09-323-867A-26
Sequence 26, Application US/09323867A
Patent No. 6506724
GENERAL INFORMATION:
APPLICANT: Amylin Pharmaceuticals, Inc.
APPLICANT: Young, Andrew et al.
TITLE OF INVENTION: USE OF EXTENDING AND AGONISTS THEREOF FOR THE TREATMENT
TITLE OF INVENTION: OF GESTATIONAL DIABETES MELLITUS
FILE REFERENCE: 030639.0032.UTL2 (243/131US)
CURRENT APPLICATION NUMBER: US/09/323.867A
CURRENT FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 189
SOFTWARE: PatentIn Ver. 2.1 and Microsoft Word
SEQ ID NO 26
LENGTH: 39
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: artificial sequence with specific variable residues
NAME/KEY: MOD.RES
LOCATION: (39)
OTHER INFORMATION: AMIDATION, Position 39 is Ser-NH2
US-09-323-867A-26

Query Match 76.0%; Score 92; DB 4; Length 39;
Best Local Similarity 65.6%; Pred. No. 7.3e-10;
Matches 21; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

DB 4 GTFTSDLSKQLEBEAVRLFVEFLKNGKGPSSGA 35

RESULT 26

US-09-323-867A-28
; Sequence 28, Application US/09323867A
; Patent No. 6506724
; GENERAL INFORMATION:
; APPLICANT: Amylin Pharmaceuticals, Inc.
; TITLE OF INVENTION: USE OF EXTENDING AND AGONISTS THEREOF FOR THE TREATMENT
; FILE REFERENCE: 030639.0032.UTL2 (243/131US)
; CURRENT APPLICATION NUMBER: US/09/323,867A
; NUMBER OF SEQ ID NOS: 189
; SOFTWARE: PatentIn Ver. 2.1 and Microsoft Word
; SEQ ID NO 28
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: artificial sequence with specific variable residues
; NAME/KEY: VARIANT
; LOCATION: (23)
; OTHER INFORMATION: Xaa at position 23 is tertiary-butylglycine
; NAME/KEY: MOD_RES
; LOCATION: (39)
; OTHER INFORMATION: AMIDATION, Position 39 is Ser-NH2
US-09-323-867A-28

Query Match 76.0%; Score 92; DB 4; Length 39;
Best Local Similarity 68.8%; Pred. No. 7.3e-10;
Matches 22; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 4 GTXXXXXSKQXEEAVRLXXXXLKNKGXSSGA 35
DB 4 GTFTSDLSKQLEBEAVRLFVEFLKNGKGPSSGA 35

RESULT 27

US-09-323-867A-30
; Sequence 30, Application US/09323867A
; Patent No. 6506724
; GENERAL INFORMATION:
; APPLICANT: Amylin Pharmaceuticals, Inc.
; TITLE OF INVENTION: USE OF EXTENDING AND AGONISTS THEREOF FOR THE TREATMENT
; FILE REFERENCE: 030639.0032.UTL2 (243/131US)
; CURRENT APPLICATION NUMBER: US/09/323,867A
; NUMBER OF SEQ ID NOS: 189
; SOFTWARE: PatentIn Ver. 2.1 and Microsoft Word
; SEQ ID NO 30
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: artificial sequence with specific variable residues
; NAME/KEY: MOD_RES
; LOCATION: (39)
; OTHER INFORMATION: AMIDATION, position 39 is Ser-NH2
US-09-323-867A-30

Query Match 76.0%; Score 92; DB 4; Length 39;
Best Local Similarity 65.6%; Pred. No. 7.3e-10;
Matches 21; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

OY 4 GTXXXXXSKQXEEAVRLXXXXLKNKGXSSGA 35
DB 4 GTFTSDLSKQLEBEAVRLFVEFLKNGKGPSSGA 35

RESULT 28
US-09-323-867A-31
; Sequence 31, Application US/09323867A
; Patent No. 6506724
; GENERAL INFORMATION:
; APPLICANT: Amylin Pharmaceuticals, Inc.
; TITLE OF INVENTION: USE OF EXTENDING AND AGONISTS THEREOF FOR THE TREATMENT
; FILE REFERENCE: 030639.0032.UTL2 (243/131US)
; CURRENT APPLICATION NUMBER: US/09/323,867A
; NUMBER OF SEQ ID NOS: 189
; SOFTWARE: PatentIn Ver. 2.1 and Microsoft Word
; SEQ ID NO 31
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: artificial sequence with specific variable residues
; NAME/KEY: VARIANT
; LOCATION: (31)
; OTHER INFORMATION: Xaa at position 31 is thiorproline
; NAME/KEY: VARIANT
; LOCATION: (36)..
; OTHER INFORMATION: Xaa at positions 36, 36, and 38 is thiorproline
; NAME/KEY: MOD_RES
; LOCATION: (39)
; OTHER INFORMATION: AMIDATION, Position 39 is Ser-NH2
US-09-323-867A-31

Query Match 76.0%; Score 92; DB 4; Length 39;
Best Local Similarity 68.8%; Pred. No. 7.3e-10;
Matches 22; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 4 GTXXXXXSKQXEEAVRLXXXXLKNKGXSSGA 35
DB 4 GTFTSDLSKQLEBEAVRLFVEFLKNGKGPSSGA 35

RESULT 29

US-09-323-867A-33
; Sequence 33, Application US/09323867A
; Patent No. 6506724
; GENERAL INFORMATION:
; APPLICANT: Amylin Pharmaceuticals, Inc.
; TITLE OF INVENTION: USE OF EXTENDING AND AGONISTS THEREOF FOR THE TREATMENT
; FILE REFERENCE: 030639.0032.UTL2 (243/131US)
; CURRENT APPLICATION NUMBER: US/09/323,867A
; NUMBER OF SEQ ID NOS: 189
; SOFTWARE: PatentIn Ver. 2.1 and Microsoft Word
; SEQ ID NO 33
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: artificial sequence with specific variable residues
; NAME/KEY: VARIANT
; LOCATION: (31)
; OTHER INFORMATION: Xaa at position 31 is homoproline
; NAME/KEY: VARIANT
; LOCATION: (36)..
; OTHER INFORMATION: Xaa at positions 36, 37, and 38 is homoproline
; NAME/KEY: MOD_RES
; LOCATION: (39)
; OTHER INFORMATION: AMIDATION, Position 39 is Ser-NH2
US-09-323-867A-33

Mon Dec 29 06:32:05 2003

US-09-889-331a-47.ral

Page 9

Query Match 76.0%; Score 92; DB 4; Length 39;
Best Local Similarity 68.8%; Pred. No. 7.3e-10;
Matches 22; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 4 GTXXXXXSKQEEAVRLXXXXLXNGXSSGA 35
DB 4 GTFTSDLSKQWEEAVRLFIEWLXNGXSSGA 35

RESULT 30
US-09-323-867A-37
Sequence 37, Application US/09323867A

Patent No. 6506724
GENERAL INFORMATION:
APPLICANT: Amylin Pharmaceuticals, Inc.
APPLICANT: Young, Andrew et al.
TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR THE TREATMENT
TITLE OF INVENTION: OF GESTATIONAL DIABETES MELLITUS
FILE REFERENCE: 030639.0032.U1L2 (243/131US)
CURRENT APPLICATION NUMBER: US/09/323,867A
CURRENT FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 189
SOFTWARE: PatentIn Ver. 2.1 and Microsoft Word
SEQ ID NO 37
LENGTH: 39
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: artificial sequence with specific variable residues
NAME/KEY: VARIANT
LOCATION: (31)
OTHER INFORMATION: Xaa at position 31 is N-methylalanine
NAME/KEY: VARIANT
LOCATION: (36)-(38)
OTHER INFORMATION: Xaa at positions 36, 37, and 38 is N-methylalanine
NAME/KEY: MOD.RES
LOCATION: (39)
OTHER INFORMATION: AMIDATION, Position 39 is Ser-NH2
US-09-323-867A-37

Query Match 76.0%; Score 92; DB 4; Length 39;
Best Local Similarity 68.8%; Pred. No. 7.3e-10;
Matches 22; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 4 GTXXXXXSKQEEAVRLXXXXLXNGXSSGA 35
DB 4 GTFTSDLSKQWEEAVRLFIEWLXNGXSSGA 35

Search completed: December 23, 2003, 10:04:28
Job time: 14.5 secs

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OM protein - protein search, using sw model

Run on: December 23, 2003, 09:59:56 ; Search time 10 Seconds
(without alignments)
186.107 Million cell updates/sec

Title: US-09-889-331A-47
Perfect score: 121
Sequence: 1 XXXGTXXXXXKQXEEAVRLXXXXLKNXGSGSGAXXXX 40
Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database: SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	91	75.2	39	1	EXE3_HELHO
2	91	75.2	87	1	EXE3_HELHO
3	42	34.7	546	1	PGW2_ECOLI
4	41	33.9	266	1	GLU1_XENLA
5	41	33.9	357	1	YAH1_SCHPO
6	41	33.9	589	1	ENCI_HUMAN
7	41	33.9	589	1	ENCI_MOUSE
8	41	33.9	2044	1	SIF1_DROME
9	41	33.9	2064	1	SIF1_DROME
10	40	33.2	1017	1	TRL3_HUMAN
11	39	32.1	341	1	HRP2_PSESY
12	38	31.4	300	1	TF2B_PYRAB
13	38	31.4	300	1	TF2B_PYRAB
14	38	31.4	355	1	NDP1_MESAU
15	38	31.4	357	1	NDP1_MOUSE
16	38	31.4	357	1	NDP1_MOUSE
17	38	31.4	419	1	NDP1_MOUSE
18	38	31.4	589	1	NDP1_MOUSE
19	37	30.6	410	1	AST2_YEAST
20	37	30.6	488	1	YKT1_CAREL
21	37	30.6	1237	1	KBP1_RABIT
22	36.5	30.2	946	1	KBP1_RABIT
23	36	29.8	318	1	NSR_LACLA
24	36	29.8	320	1	FEZ2_HUMAN
25	36	29.8	324	1	FEZ2_HUMAN
26	36	29.8	324	1	GLXA_RHIME
27	36	29.8	324	1	VP35_VACCC
28	36	29.8	325	1	VP35_VACCC
29	36	29.8	373	1	VP35_VACCC
30	36	29.8	401	1	CPXP_BRAVA
31	36	29.8	413	1	FL1_TOBAC
32	36	29.8	472	1	XYLA_ARATH
33	36	29.8	633	1	STHR_RHIME

34	36	29.8	717	1	U848_HUMAN	Q9uh93 homo sapien
35	36	29.8	730	1	HELS_METMA	Q8pz77 metanosarc
36	36	29.8	845	1	SCPI_MESAU	Q60563 mesocricetu
37	36	29.8	1049	1	CAR1_SUITAU	Q970u7 suillolobus
38	36	29.8	3068	1	POLC_PEMVIC	Q01500 p genome po
39	36	29.8	4473	1	PLE1_CRICR	Q91155 cricetus
40	36	29.8	4684	1	PLE1_HUMAN	Q15149 homo sapien
41	36	29.8	4687	1	PLE1_RAT	Q10427 ratu
42	36	29.8	5938	1	MAC4_HUMAN	Q96242 homo sapien
43	35.5	29.3	111	1	HMGZ_DROME	Q06943 drosophila
44	35.5	29.3	312	1	MOCH_CHLTE	Q59014 chlorobium
45	35	28.9	229	1	COX2_MXGGL	P55045 myxine glut
46	35	28.9	273	1	PPG_STRMU	P55045 streptococc
47	35	28.9	275	1	PPG_STRP3	Q88480 streptococc
48	35	28.9	275	1	PPG_STRP8	Q88250 streptococc
49	35	28.9	275	1	PPG_STRP8	Q9a131 streptococc
50	35	28.9	300	1	TF2B_PYRPU	P29095 pyrococcus

ALIGNMENTS

RESULT 1
EXE3_HELHO STANDARD; PRT; 39 AA.

AC P20394:1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Extendin-3.
OS Heloderma horridum horridum (Mexican beaded lizard).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosaurs; Squamata; Scleroglossa; Anguilliformes; Helodermatidae;
OC Heloderma.
OX NCBI_TaxID=8552;
RN [1]
RP TISSUE=Venom;
RC MEDLINE=91056067; PubMed=1700785;
RA Eng J.; Andrew P.C.; Kleinman W.A.; Singh L.; Rautman J.-P.;
RT "Purification and structure of extendin-3, a new pancreatic
secretagogue isolated from Heloderma horridum venom."
RL J. Biol. Chem. 265:20259-20262(1990).
CC -1- FUNCTION: Has a VIP/secretin-like biological activity. Interacts
with the extendin receptor.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -1- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
DR HSP; A23674; HG43Z.
DR InterPro; IPR000532; Glucagon.
DR Pfam; PF00123; hormone2; 1.
DR SMART; SM00070; GLUCA; 1.
DR PROSITE; PS00260; GLUCAGON; 1.
KM Glucagon family; Toxin; Amidation.
FT MOD_RES 39
SQ SEQUENCE 39 AA; 4204 MW; A44251D3A4B1D1B9 CRC64;
Query Match 75.2%; Score 91; DB 1; Length 39;
Best Local Similarity 65.6%; Pred. No. 6.6e-10;
Matches 21; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

DR Pfam: PF02879; PGM_PMM_11; 1.
 DR Pfam: PF02880; PGM_PMM_11; 1.
 DR TIGR: TIGR01132; PGM_1.
 DR PROSITE: PS00710; PGM_PMM_1.
 DR Isoemase: Phosphorylation; Complete proteome.
 FT ACT_SITE 146 146
 (BY SIMILARITY).
 FT PHOSPHOSERINE INTERMEDIATE
 FT
 SQ SEQUENCE 546 AA; 58361 MM; 666B89C2F2EC059 CRC64;
 Query Match 34.7%; Score 42; DB 1; Length 546;
 Best Local Similarity 52.9%; Pred. NO. 6.9; Indels 0; Gaps 0;
 Matches 9; Conservative 2; Mismatches 6

QY 12 KQEEBNAVRLXXXXLN 28
 DB 529 KQEEBNAVRLXXXXLN 545

RESULT 4
 ID GLU1_XENLA STANDARD; PRT; 266 AA.
 AC 042143;
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Glucagon I precursor (Contains: Glucagon-like peptide 1A
 (GLP-1A); Glucagon-like peptide 1B (GLP-1B); Glucagon-like peptide 1C
 (GLP-1C); Glucagon-like peptide 2 (GLP-2)).
 DE (GLP-1C); Glucagon-like peptide 2 (GLP-2)).
 OS Xenopus laevis (African clawed frog).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
 OC Xenopodidae; Xenopus.
 OC NCBI_TaxID=8335;
 RN (1)
 RP TISSUE=Pancreas; PubMed=9223287;
 RX MEDLINE=97368292; Pubmed=9223287;
 RA Irwin D.M., Satkunaratnam M., Wen Y., Brubaker P.L., Pederson R.A.,
 Wheeler M.B.;
 RT "The Xenopus glucagon gene encodes novel GLP-1-like peptides with
 insulinotropic properties.";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:7915-7920(1997).
 CC -1- FUNCTION: Promotes hydrolysis of glycogen and lipids, and raises
 the blood sugar level.
 CC -1- FUNCTION: Promotes hydrolysis of glycogen and lipids, and raises
 the blood sugar level.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=C042143-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=C042143-2; Sequence=VSP_001755;
 CC -1- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
 CC -1- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
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 CC
 CC EMBL: AF004432; AAB55660.1;
 DR HSSP: P01274; IGCN.
 DR InterPro: IPR000532; Glucagon.
 DR Pfam: PF00123; hormone2; 5.
 DR PRINTS: PR00275; GLUCAGON.
 DR SMART: SM00707; GLUCA; 5.
 DR PROSITE: PS00260; GLUCAGON; 5.
 DR Glucagon family; Hormone; Signal; Cleavage on pair of basic residues;
 KW Multigene family; Alternative splicing.
 FT SIGNAL 1 20
 FT PROPEP 21 50 GLUCAGON.
 FT PEPTIDE 53 81
 FT PROPEP 84 95

FT PEPTIDE 97 133 GLUCAGON-LIKE PEPTIDE 1A.
 FT PROPEP 136 140 GLUCAGON-LIKE PEPTIDE 1B.
 FT PEPTIDE 142 172 GLUCAGON-LIKE PEPTIDE 1C.
 FT PROPEP 175 178 GLUCAGON-LIKE PEPTIDE 1C.
 FT PEPTIDE 180 210 GLUCAGON-LIKE PEPTIDE 2.
 FT PROPEP 213 224 GLUCAGON-LIKE PEPTIDE 2.
 FT PEPTIDE 227 259
 FT PROPEP 261 266
 FT VARSPLIC 214 261
 FT
 SQ SEQUENCE 266 AA; 30951 MM; 544F7BB20AF872C CRC64;
 Query Match 33.9%; Score 41; DB 1; Length 266;
 Best Local Similarity 34.5%; Pred. NO. 5;
 Matches 10; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

QY 4 GTXXXXXKQEEBNAVRLXXXXLN 32
 DB 100 GTFTSDVTQDLDEKAKERFDMLNGAPS 128

RESULT 5
 ID YAUH_SCHPO STANDARD; PRT; 357 AA.
 AC 010170; Q9Y717;
 DT 15-OCT-1996 (Rel. 34, Created)
 DT 15-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-OCT-2001 (Rel. 40, Last annotation update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Hypothetical protein C26A3.17c in chromosome 1.
 DE SPAC26A3.17C OR SPAC8E11.11.
 GN SPAC26A3.17C OR SPAC8E11.11.
 OS Schizosaccharomyces pombe (fission yeast).
 OS Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OC NCBI_TaxID=4896;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=21848401; Pubmed=11859360;
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 Seguros J., Peat N., Hayles J., Baker S., Baaham D., Bowman S.,
 Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 Collins M., Connor R., Cronin A., Davis P., Felwell T., Fraser A.,
 Gentles S., Goble A., Hamlin N., Harris P., Hildalgo J., Hodgson G.,
 Holtroyd S., Hornsby T., Howarth S., Huxley E.J., Hunt S., Jagels K.,
 James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 Mooney P., Moule S., Pearson D., Quail M.A., Rabinowitsch E.,
 Oliver K., O'Neill S., Saunders D., Seeger K., Sharp S.,
 Rutherford K., Rutter S., Squares R., Squares S., Stevens K.,
 Skelton J., Smmonds M., Squares R., Squares S., Warren T., Whitehead S.,
 Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 Woodward J., Volkart G., Aert R., Roben J., Grymberg B.,
 Weljens I., Vantrelle G., Rieger M., Scheider M., Mueller-Auer S.,
 Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
 Borzym K., Langer I., Beck A., Lehnach H., Reinhardt R., Pohl T.M.,
 Eger P., Zimmermann M., Wedler H., Gloux S., Lelaire V., Mottier S.,
 Goffeau A., Cadieu E., Dreano S., Hunt C., Moore K., Hurst S.M.,
 Galibert F., Aves S.J., Xiang Z., Tallada V.A., Garçon A., Thode G.,
 Lucifora M., Rochet M., Galliard C., Tallada V.A., Garçon A., Thode G.,
 Daga R.R., Crusado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 Riera R.R., Revuelta J.L., Moreno S., Armerstrong J., Forsberg S.L.,
 Dominguez A., Revuelta J.L., Moreno S., Armerstrong J., Forsberg S.L.,
 Cerutti L., Lowe T., McCombie W.R., Paulsen O., Potholkin J.,
 Shpakovski G.V., Uesery D., Barrett B.G., Nurse P.,
 Nature 415:871-880(2002).
 RT Nature 415:871-880(2002).
 CC -1- SIMILARITY: SOME, TO RAT GUANIDINOCYTRATE N-METHYLTRANSFERASE.
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CC -----

DR EMBL: AL021817; CAB40198.1; -

DR EMBL: Z69240; CA93240.1; -

DR GeneDB Spombe: SPAC26A3.17c; -

DR InterPro: IPR002110; ANK

DR PROSITE: PS50287; ANK_REPEAT_REGION; UNKNOWN_1

DR Hypothetical protein.

KM SEQUENCE 357 AA; 40709 MW; 552988D3B88D91A9 CRC64;

Query March 33.9%; Score 41; DB 1; Length 357;

Best Local Similarity 44.8%; Pred. No. 6.8;

Matches 8; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 12 KQEEVRLXXXXLNGKSSG 34

Db 64 KETEVQAEVTKWILNSGVWNG 86

RESULT 6

ENCL HUMAN STANDARD; PRT; 589 AA.

ID ENCL_HUMAN

AC 014682; 075464; Q9UG99;

DT 30-MAY-2000 (Rel. 39, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Ectoderm-neural cortex-1 protein (ENC-1) (P53-induced protein 10)

DE (Nuclear matrix protein NRP/B).

DE ENCL OR P1010 OR NRPB.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OC NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Colon cancer;

RC MEDLINE=97449378; PubMed=9305847;

RA Polyak K., Xia Y., Zweier J.L., Kinzler K.W., Vogelstein B.;

RA "A model for p53-induced apoptosis."

RL Nature 389:300-305 (1997).

RN [2]

RP SEQUENCE FROM N.A.

RC MEDLINE=98350113; PubMed=968334;

RA Hernandez M.-C., Andres-Barquin P.J., Holt I., Israel M.A.;

RA "Cloning of human ENC-1 and evaluation of its expression and

RA regulation in nervous system tumors."

RL Exp. Cell Res. 242:470-477 (1998).

RN [3]

RP SEQUENCE FROM N.A.

RC TISSUE=Fetal brain, and Hippocampus;

RC MEDLINE=98234394; PubMed=9566959;

RA Kim T.-A., Lim J., Oca S., Raja S., Rogers R., Rivnay B., Avraham H.;

RA Avraham S.;

RA "NRP/B, a novel nuclear matrix protein, associates with p10(RB) and

RA is involved in neuronal differentiation."

RL J. Cell Biol. 141:553-566 (1998).

RN [4]

RP SEQUENCE FROM N.A.

RC TISSUE=Muscle;

RC MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.;

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.;

RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.;

RA Hopkins R.F., Jordan H., Moore T., Wax S.L., Wang J., Hsieh F.;

RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.;

RA Sapien M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.;

RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.;

RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.;

RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.;

RA Richards S., Wotley K.C., Hale S., Garcia A.M., Gay L.J., Huliy S.W.;

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gabbe R.A.;

RA Fahy J., Helton E., Kettman W., Madan A., Rodriguez S., Sanchez A.;

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.;

RA Blakesley R.M., Touchman J.W., Green E.D., Dickson M.C.;

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.;

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.;

RA Scherich A., Schein J.E., Jones S.J.M., Maiz A.A.;

RT "Generation and initial analysis of more than 15,000 full-length

RT human and mouse cDNA sequences."

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

CC -1- FUNCTION: ACTIN-BINDING PROTEIN INVOLVED IN THE REGULATION OF

CC NEURONAL PROCESS FORMATION AND IN DIFFERENTIATION OF NEURAL CREST

CC CELLS. MAY BE DOWN-REGULATED IN NEUROBLASTOMA TUMORS.

CC -1- SUBUNIT: BINDS TO R1. HYPOPHOSPHORYLATED R1 ASSOCIATES WITH ENCL

CC ASSOCIATES WITH ENCL IN NONDIFFERENTIATING CELLS.

CC -1- SUBCELLULAR LOCATION: NUCLEAR. NUCLEAR MATRIX-ASSOCIATED.

CC EXPRESSION IN FETAL HEART, LUNG AND KIDNEY. HIGHLY EXPRESSED IN

CC ADULT BRAIN, PARTICULARLY HIGH IN THE HIPPOCAMPUS AND

CC AMYGDALA, AND SPINAL CHORD. DETECTABLE IN ADULT PANCREAS.

CC -1- DEVELOPMENTAL STAGE: DRAMATICALLY UPREGULATED UPON NEURONAL

CC DIFFERENTIATION.

CC -1- PTM: PHOSPHORYLATED.

CC -1- SIMILARITY: Contains 1 BTB/POZ domain.

CC -1- SIMILARITY: Contains 6 Kelch repeats.

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CC -----

DR EMBL: AF010314; AAC39532.1; -

DR EMBL: AF005381; AAC64498.1; -

DR EMBL: AF059611; AAC26109.1; -

DR EMBL: BC000418; AA000418.1; -

DR Genew; HGNC:3345; ENCL.

DR MIM; 605173; -

DR GO; GO:0005634; C:nucleus; TAS.

DR GO; GO:0007275; P:development; TAS.

DR GO; GO:0007399; P:neurogenesis; TAS.

DR InterPro: IPR000210; BTB_POZ.

DR InterPro: IPR006652; Kelch_rep.

DR Pfam; PF00651; BTB_1.

DR Pfam; PF01344; Kelch; 5.

DR SMART; SM00225; BTB; 1.

DR SMART; SM00612; Kelch; 6.

DR PROSITE; PS50097; BTB; 1.

KM Actin-binding; Developmental protein; Cytoskeleton; Kelch repeat;

KM Repeat; Phosphorylation.

FT DOMAIN 46 114

FT REPEAT 296 340

FT REPEAT 341 388

FT REPEAT 389 444

FT REPEAT 446 492

FT REPEAT 494 538

FT REPEAT 539 580

FT CONFLICT 112 135

FT CONFLICT 237 238

FT CONFLICT 402 402

FT CONFLICT 427 427

FT CONFLICT 430 438

FT CONFLICT 484 589

SEQUENCE 589 AA; 66129 MW; DB003ADP65BAAO CRC64;

Query Match 33.9%; Score 41; DB 1; Length 589;

Best Local Similarity 45.0%; Pred. No. 11;

Matches 9; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

BTB.

KELCH 1.

KELCH 2.

KELCH 3.

KELCH 4.

KELCH 5.

KELCH 6.

INEEMASLEAGDMLEFQ -> HQLEGKGRNSLLGSLVTC

MSRF (IN REF. 1).

RL -> TR (IN REF. 1).

C -> S (IN REF. 2).

V -> A (IN REF. 1).

LREVSUNA -> RPRRRYNAQ (IN REF. 1).

YTAALVGNQIFVIGDTEFAGAGYFNSFTYVWGV

TAKMSCHAVASGKLVYGGVFGIORCKTLDCYDPLDV

NSITTPYSILPTAFVSTWKLPS -> IHSQASPGQTOP

FLVGVNFSACRCL (IN REF. 1).

QY 11 SKOXEEAVRLXXXXKNG 30
DB 262 SKXIVEAIRCKLKLQNDG 281

RESULT 7

ENCL_MOUSE STANDARD; PRT: 589 AA.
ID ENCL_MOUSE
AC 035709
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ectoderm-neural cortex-1 protein (ENC-1).
GN ENCL OR ENC-1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Swiss albino; TISSUE=Brain;
RX MEDLINE=97252647; PubMed=9096139;
RA Hernandez M.-C., Andres-Barguin P.J., Martinez S., Bulfone A.,
RA Rubenstein J.L.R., Israel M.A., Martinez S., Bulfone A.,
RT "ENC-1, a novel mammalian kelch-related gene specifically expressed in
the nervous system encodes an actin-binding protein.";
RL J. Neurosci. 17:3038-3051(1997).
CC -1- FUNCTION: ACTIN-BINDING PROTEIN INVOLVED IN THE REGULATION OF
NEURONAL PROCESS FORMATION AND IN DIFFERENTIATION OF NEURAL CREST
CELLS.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC. INTERACTS WITH THE ACTIN
CYTOSKELETON.
CC -1- TISSUE SPECIFICITY: PRIMARILY EXPRESSED IN THE NERVOUS SYSTEM.
CC -1- DEVELOPMENTAL STAGE: EXPRESSION IS HIGHLY DYNAMIC BUT MOSTLY
RESTRICTED TO THE NS. OUTSIDE THE NS, EXPRESSION IS DETECTED IN
THE POSTRAL-MOST SOMITOMERE OF THE PRESOMITIC MESODERM. AT THE
TIMES CORRESPONDING TO THE EPITHELIALIZATION THAT PRECEDES SOMITE
FORMATION. FIRST DETECTED IN THE BRAIN AND SPINAL CHORD OF 12 PC
EMBRYOS.
CC -1- SIMILARITY: Contains 1 BTB/POZ domain.
CC -1- SIMILARITY: Contains 6 Kelch repeats.
CC -----
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CC -----
DR EMBL: U65079; AB64206.1; -
DR MGD: MGI:109610; Encl.
DR InterPro: IPR000210; BTB_POZ.
DR InterPro: IPR006652; Kelch_rep.
DR Pfam: PF00651; BTB, 1.
DR Pfam: PF01344; Kelch, 5.
DR SMART: SM00225; BTB, 1.
DR SMART: SM00612; Kelch, 6.
DR PROSITE: PS50097; BTB, 1.
KW Actin-binding; Developmental protein; Cytoskeleton; Kelch repeat;
KW Repeat.
FT DOMAIN 46 114 BTB.
FT REPEAT 296 340 KELCH 1.
FT REPEAT 341 388 KELCH 2.
FT REPEAT 389 444 KELCH 3.
FT REPEAT 446 492 KELCH 4.
FT REPEAT 494 538 KELCH 5.
FT REPEAT 539 585 KELCH 6.
SQ SEQUENCE 589 AA; 66085 MW; 12E62354D508B6A2 CRC64;

Query Match 33.9%; Score 41; DB 1; Length 589;
Best Local Similarity 45.0%; Pred. No. 11;
Matches 9; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 11 SKOXEEAVRLXXXXKNG 30
DB 262 SKXIVEAIRCKLKLQNDG 281

RESULT 8

SIF2_DROME STANDARD; PRT: 2044 AA.
ID SIF2_DROME
AC P01620
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Still life protein type 2 (SIF type 2).
GN SIF.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Head;
RX MEDLINE=97153054; PubMed=8999801;
RA Some M., Hoshino M., Suzuki E., Kuroda S., Kaibuchi K., Nakagoshi H.,
RA Saigo K., Nabeshima Y.-I., Hama C.,
RT "Still life, a protein in synaptic terminals of Drosophila homologous
to GTP-exchange factors.";
RL Science 275:543-547(1997).
RN [2]
RP ERRATUM.
RA Some M., Hoshino M., Suzuki E., Kuroda S., Kaibuchi K., Nakagoshi H.,
RA Saigo K., Nabeshima Y.-I., Hama C.,
RL Science 275:1405-1405(1997).
CC -1- FUNCTION: REGULATES SYNAPTIC DIFFERENTIATION THROUGH THE
ORGANIZATION OF ACTIN CYTOSKELETON POSSIBLY BY ACTIVATING RHO-LIKE
GTPASES. IS LIKELY A FACTOR IN THE CASCADE OF RAC1 OR CDC42 IN THE
NEURONS.
CC -1- SUBCELLULAR LOCATION: LOCALIZES TO THE SUBMEMBRANOUS REGION OF
SYNAPTIC TERMINALS.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1P type 2;
CC IsoId=P01620-1; Sequence=Displayed;
CC Name=SIF type 1;
CC IsoId=P01621-1; Sequence=External;
CC -1- DEVELOPMENTAL STAGE: AT STAGE 14, EXPRESSION OCCURS IN EACH
SEGMENT OF THE CENTRAL NERVOUS SYSTEM. AT STAGE 17, EXPRESSION
BECOMES RESTRICTED TO THE SYNAPTIC REGIONS OF THE BRAIN AND
VENTRAL NERVE CORD, WHERE SYNAPSES UNDERGO MATURATION.
CC -1- SIMILARITY: Contains 1 DBL-homology (DH) domain.
CC -1- SIMILARITY: Contains 1 PDZ/DHR domain.
CC -1- SIMILARITY: Contains 1 Ras-binding (RBD) domain.
CC -1- SIMILARITY: Contains 2 PH domains.
CC -----
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CC -----
DR EMBL: D86546; BAA1308.1; -
DR PIR: T13704; T13704.
DR HSSP: P08567; 1PIS.
DR FlyBase: FBgn019652; sif
DR InterPro: IPR001331; GDS_CDC24.
DR InterPro: IPR001478; PDZ.
DR InterPro: IPR001849; PH.
DR InterPro: IPR003116; RBD.
DR InterPro: IPR000219; RhodGEF.
DR Pfam: PF00169; PH, 1.

DR Pfam: PF002196; RBD; 1.
 DR SMART: SM00228; PDZ; 1.
 DR SMART: SM00233; PH; 2.
 DR SMART: SM00455; RBD; 1.
 DR SMART: SM00325; RhogEF; 1.
 DR PROSITE: PS00741; DH 1; 1.
 DR PROSITE: PS50010; DH 2; 1.
 DR PROSITE: PS50106; PDZ; 1.
 DR PROSITE: PS50003; PH DOMAIN; 1.
 DR PROSITE: PS50898; RBD; 1.
 DR Guanine-nucleotide releasing factor; Developmental protein; Synapse;
 KW Repeat; Alternative splicing.
 FT DOMAIN 62 249
 FT REPEAT 62 86
 FT REPEAT 94 118
 FT REPEAT 154 178
 FT REPEAT 225 249
 FT DOMAIN 819 937
 FT DOMAIN 1101 1168
 FT DOMAIN 1184 1273
 FT DOMAIN 1408 1602
 FT DOMAIN 1674 1767
 FT DOMAIN 467 470
 FT DOMAIN 646 649
 FT DOMAIN 1295 1298
 FT DOMAIN 1898 1909
 FT DOMAIN 1929 1933
 SQ SEQUENCE 2044 AA; 228324 MW; 75D7CF21F49654B6 CRC64;

Query Match 33.9%; Score 41; DB 1; Length 2044;
 Best Local Similarity 41.7%; Pred. No. 41;
 Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

OY 12 KQXEEAVRLXXXXLKGXSSGA 35
 Db 1761 RQIIRSVNMSIPKMGSSGS 1784

RESULT 9
 ID SIF1_DROME STANDARD; PRT; 2064 AA.
 AC P91621;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Still life protein type 1 (SIF type 1).
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OC NCBI TaxID=7227;
 OX [1]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Head;
 RA MEDLINE=9713054; Pubmed=8999801;
 RA Some M., Hoshino M., Suzuki E., Kuroda S., Kaibuchi K., Nakagoshi H.,
 RA Saigo K., Nabeshima Y.-I., Hama C.;
 RT "Still life, a protein in synaptic terminals of Drosophila homologous
 RT to GDP-GTP exchangers.";
 RL Science 275:543-547 (1997).
 RN [2]
 RP ERRATUM.
 RA Some M., Hoshino M., Suzuki E., Kuroda S., Kaibuchi K., Nakagoshi H.,
 RA Saigo K., Nabeshima Y.-I., Hama C.;
 RL Science 275:1405-1405 (1997).
 CC -1- FUNCTION: REGULATES SYNAPTIC DIFFERENTIATION THROUGH THE
 CC ORGANIZATION OF ACTIN CYTOSKELETON POSSIBLY BY ACTIVATING RHO-LIKE
 CC GTPASES. IS LIKELY A FACTOR IN THE CASCADE OF RAC1 OR CDC42 IN THE
 CC NEURONS.
 CC -1- SUBCELLULAR LOCATION: LOCALIZES TO THE SUBMEMBRANOUS REGION OF
 CC SYNAPTIC TERMINALS.

CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=SIF type 1;
 CC IsoId=P91621-1; Sequence=Displayed;
 CC Name=SIF type 2;
 CC IsoId=P91620-1; Sequence=External;
 CC -1- DEVELOPMENTAL STAGE: AT STAGE 14, EXPRESSION OCCURS IN EACH
 CC SEGMENT OF THE CENTRAL NERVOUS SYSTEM. AT STAGE 17, EXPRESSION
 CC BECOMES RESTRICTED TO THE SYNAPTIC REGIONS OF THE BRAIN AND
 CC VENTRAL NERVE CORD, WHERE SYNAPSES UNDERGO MATURATION.
 CC -1- SIMILARITY: Contains 1 DBL-homology (DH) domain.
 CC -1- SIMILARITY: Contains 1 PDZ/DHR domain.
 CC -1- SIMILARITY: Contains 2 PH domains.
 CC -1- SIMILARITY: Contains 1 Ras-binding (RBD) domain.
 CC -----
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 CC -----
 CC EMBL: D86547; BAA13109.1; -
 CC PIR: T13707; T13707.
 CC HSP: P08567; 1PLS.
 CC FlyBase: FBgn0019652; sif.
 CC InterPro: IPR001331; GDS_CDC24.
 CC InterPro: IPR001478; PDZ.
 CC InterPro: IPR001849; PH.
 CC InterPro: IPR003116; RBD.
 CC InterPro: IPR000219; RhogEF.
 CC InterPro: IPR001960; WH1.
 DR Pfam: PF00169; PH; 1.
 DR Pfam: PF00196; RBD; 1.
 DR Pfam: PF00621; RhogEF; 1.
 DR SMART: SM00228; PDZ; 1.
 DR SMART: SM00233; PH; 2.
 DR SMART: SM00455; RBD; 1.
 DR SMART: SM00325; RhogEF; 1.
 DR SMART: SM00461; WH1; 1.
 DR PROSITE: PS00741; DH 1; 1.
 DR PROSITE: PS50010; DH 2; 1.
 DR PROSITE: PS50106; PDZ; 1.
 DR PROSITE: PS50898; RBD; 1.
 DR Guanine-nucleotide releasing factor; Developmental protein; Repeat;
 KW Myristate; Synapse; Alternative splicing.
 FT DOMAIN 839 957
 FT DOMAIN 1121 1188
 FT DOMAIN 1204 1293
 FT DOMAIN 1428 1622
 FT DOMAIN 1694 1787
 FT DOMAIN 445 453
 FT DOMAIN 545 548
 FT DOMAIN 1315 1318
 FT DOMAIN 1918 1929
 FT DOMAIN 1949 1953
 FT LIPID 2
 SQ SEQUENCE 2064 AA; 230489 MW; D3BDC10A9D956C CRC64;

Query Match 33.9%; Score 41; DB 1; Length 2064;
 Best Local Similarity 41.7%; Pred. No. 42;
 Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

OY 12 KQXEEAVRLXXXXLKGXSSGA 35
 Db 1761 RQIIRSVNMSIPKMGSSGS 1804

RESULT 10
 ID TRJ3_HUMAN STANDARD; PRT; 1017 AA.

```

AC O9HCF6;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Long transient receptor potential channel 3 (TRP3) (Fragment).
GN TRPM3 OR LTRPC3 OR KIA1616.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA MEDLINE=20450683; PubMed=1097877;
RA Nagase T., Kikuno R., Nakayama M., Hirose M., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes.
RT XVIII. The complete sequences of 100 new cDNA clones from brain which
RT code for large proteins in vitro."
RL DNA Res. 7:273-281(2000).
CC -1- FUNCTION: MAY BE A CALCIUM CHANNEL.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC -1- SIMILARITY: BELONGS TO THE TRANSIENT RECEPTOR FAMILY. LTRPC
CC SUBFAMILY.
CC -----
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CC -----
DR EMBL: AB046836; BAB3442.1; -
DR GenBank: HGNC:17992; TRPM3.
DR InterPro: IPR002111; Cat_channel_Trp.
DR InterPro: IPR005821; Ion_trans.
DR Pfam: PF00520; Ion_trans; 1.
KM Ionic channel; Transmembrane; Ion transport; Calcium channel.
FT NON_TER 1
FT TRANSMEM 80 100 POTENTIAL.
FT TRANSMEM 183 203 POTENTIAL.
FT TRANSMEM 250 270 POTENTIAL.
FT TRANSMEM 314 334 POTENTIAL.
FT TRANSMEM 402 422 POTENTIAL.
FT TRANSMEM 453 473 POTENTIAL.
SQ SEQUENCE 1017 AA; 116681 MW; B088354F100A972C CRC64;

Query Match 33.1%; Score 40; DB 1; Length 1017;
Best Local Similarity 39.1%; Pred. No. 30;
Matches 9; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

OY 11 SKOXEEAVRLXXXXLKGGSS 33
DB 129 TKKEEDMELTAMLRGNSS 151

RESULT 11
HRP2_PSSY
ID_HRP2_PSSY STANDARD; PRT; 341 AA.
AC P35674;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Harpin-PSS.
GN Harpin.
OS Pseudomonas syringae (pv. syringae).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OC NCBI_TaxID=321;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 141-162.
RC STRAIN=61;
RX MEDLINE=93313957; PubMed=8324821;

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RA He S.Y., Huang H.-C., Collmer A.;
RT "Pseudomonas syringae pv. syringae harpinPss: a protein that is
RT secreted via the Hrp pathway and elicits the hypersensitive response
RT in plants."
RL Cell 73:1255-1266(1993).
CC -1- FUNCTION: ELICITS THE HYPERSENSITIVE RESPONSE (HR) IN THE PLANT
CC UPON INFECTION. HARPIN ELICITS HR IN NON-HOSTS AND IS ALSO
CC REQUIRED FOR PATHOGENICITY IN HOST PLANTS.
CC -1- SUBCELLULAR LOCATION: SECRETED; VIA THE HRP SECRETION PATHWAY.
CC -1- MISCELLANEOUS: DIFFERENT PLANTS EXHIBIT DIFFERENT LEVELS OF
CC SENSITIVITY TO HARPIN-PSS.
CC -----
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CC -----
DR EMBL: L14775; AAA25839.1; -
DR PIR: A40706; A40706
DR InterPro: IPR006961; Hrp2.
DR Pfam: PF04877; Hrp2; 1.
KM Hypersensitive response; Repeat.
FT DOMAIN 210 271 2 X 7 AA REPEATS OF G-G-G-L-G-T-P.
FT REPEAT 210 216 1-1.
FT REPEAT 265 271 1-2.
FT DOMAIN 276 314 2 X 4 AA REPEATS OF Q-T-G-T.
FT REPEAT 276 279 2-1.
FT REPEAT 311 314 2-2.
SQ SEQUENCE 341 AA; 34721 MW; 75FB7329B5380179 CRC64;

Query Match 32.2%; Score 39; DB 1; Length 341;
Best Local Similarity 32.0%; Pred. No. 15;
Matches 8; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

OY 5 TXXXXSKOXEEAVRLXXXXLNG 29
DB 27 TTGSTSSKALQEVVYVLAELMRNG 51

RESULT 12
TF2B_PYPAB
ID_TF2B_PYPAB STANDARD; PRT; 300 AA.
AC Q9V0V5;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Transcription initiation factor IIB (TFIIB).
GN TFB OR PYRA06850 OR PAB1912.
OS Pyrococcus abyssi.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OC NCBI_TaxID=29292;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GBS / O'reay;
RX PubMed=12622808;
RA Cohen G.N., Barde V., Flament D., Galperin M., Hellig R., Lecompte O.,
RA Poch O., Prieur D., Querellon J., Ripp R., Thierry J.-C.,
RA Van der Oost J., Weisenbach J., Zivanovic V., Forterre P.;
RT "An integrated analysis of the genome of the hyperthermophilic
RT archaeon Pyrococcus abyssi."
RL Mol. Microbiol. 47:1495-1512(2003)
CC -1- FUNCTION: STABILIZES TBP BINDING TO AN ARCHAEAL BOX-A PROMOTER.
CC ALSO RESPONSIBLE FOR RECRUITING RNA POLYMERASE II TO THE PRE-
CC INITIATION COMPLEX (DNA-TBP-TFIIB) (BY SIMILARITY).
CC -1- COFACTOR: Binds 1 zinc ion per subunit (BY SIMILARITY).
CC -1- SIMILARITY: Belongs to the TFIIB family.
CC -----
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DR EMBL: AJ248285; CAB49598.1; -
 DR PIR: E75110; E75110.
 DR HSSP: P29095; 1A1S.
 DR HAMAP: MF_00383; -; 1.
 DR InterPro: IPR006670; Cyclin.
 DR InterPro: IPR000812; TFIIB euk.
 DR Pfam: PF00382; transcript_Fac2; 2.
 DR PRINTS: PR00685; TIFACTOR1B.
 DR SMART: SM00385; CYCLIN; 2.
 DR PROSITE: PS00782; TFIIB; 2.
 DR Transcription regulation; Repeat; Zinc-finger; Metal-binding; Zinc;
 KW Complete proteome.
 FT ZN FING 7 29 ZN-RIBBON TFIIB-TYPE.
 FT REPEAT 114 197 1.
 FT REPEAT 210 291 2.
 FT METAL 7 7 ZINC (BY SIMILARITY).
 FT METAL 10 10 ZINC (BY SIMILARITY).
 FT METAL 26 26 ZINC (BY SIMILARITY).
 FT METAL 29 29 ZINC (BY SIMILARITY).
 SQ SEQUENCE 300 AA; 34069 MW; D7AE15181A36BD4F CRC64;

Query Match 31.4%; Score 38; DB 1; Length 300;
 Best Local Similarity 44.4%; Pred. No. 20;
 Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

OY 12 KQXEEAVRLXXXXLXNG 29
 Db 127 KXVEEAPARLYREAVRKG 144

RESULT 13
 TF2B-PYRHO STANDARD; PRT; 300 AA.
 ID TF2B-PYRHO
 AC 059151;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Transcription initiation factor IIB (TFIIB).
 GN TFB OR PH1482
 OS Pyrococcus horikoshii
 OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
 OC Pyrococcus.
 OC NCBI_TaxID=53953;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=OT3;
 RX MEDLINE=96344137; Pubmed=9679194;
 RA Kawarabayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
 RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyma A., Nagai Y.,
 RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamizu M., Ohfuku Y.,
 RA Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushiida N., Oguchi A.,
 RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
 RA Mesucl Y., Shizuya H., Kikuchi H.;
 RT "Complete sequence and gene organization of the genome of a hyper-
 RT thermophilic archaeobacterium, Pyrococcus horikoshii OT3";
 RL DNA Res. 5:55-66(1998).
 CC -1- FUNCTION: STABILIZES TBP BINDING TO AN ARCHAEAL BOX-A PROMOTER.
 CC -1- ALSO RESPONSIBLE FOR RECRUITING RNA POLYMERASE II TO THE PRE-
 CC INITIATION COMPLEX (DNA-TBP-TFIIB) (BY SIMILARITY).
 CC -1- SIMILARITY: Belongs to the TFIIB family.

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DR EMBL: AP000006; BA330589.1; -
 DR PIR: E71023; E71023.
 DR HSSP: P29095; 1A1S.
 DR HAMAP: MF_00383; -; 1.
 DR InterPro: IPR006670; Cyclin.
 DR InterPro: IPR000812; TFIIB euk.
 DR Pfam: PF00382; transcript_Fac2; 2.
 DR PRINTS: PR00685; TIFACTOR1B.
 DR SMART: SM00385; CYCLIN; 2.
 DR PROSITE: PS00782; TFIIB; 2.
 DR Transcription regulation; Repeat; Zinc-finger; Metal-binding; Zinc;
 KW Complete proteome.
 FT ZN FING 7 29 ZN-RIBBON TFIIB-TYPE.
 FT REPEAT 114 197 1.
 FT REPEAT 210 291 2.
 FT METAL 7 7 ZINC (BY SIMILARITY).
 FT METAL 10 10 ZINC (BY SIMILARITY).
 FT METAL 26 26 ZINC (BY SIMILARITY).
 FT METAL 29 29 ZINC (BY SIMILARITY).
 SQ SEQUENCE 300 AA; 34097 MW; DE9758F398BC855F CRC64;

Query Match 31.4%; Score 38; DB 1; Length 300;
 Best Local Similarity 44.4%; Pred. No. 20;
 Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

OY 12 KQXEEAVRLXXXXLXNG 29
 Db 127 KXVEEAPARLYREAVRKG 144

RESULT 14
 NDPI_MESAU STANDARD; PRT; 355 AA.
 ID NDPI_MESAU
 AC Q60430;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Neurogenic differentiation factor 1 (Neurod1) (Beta-cell E-box trans-
 DE activator 2) (BETA2).
 GN NEUROD1 OR NEUROD.
 OS Mesocricetus auratus (Golden hamster).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Mesocricetus.
 OC NCBI_TaxID=10036;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9529322; Pubmed=7774807;
 RA Naya F.J., Steilrecht C.M.M., Tsai M.-J.;
 RT "Tissue-specific regulation of the insulin gene by a novel basic
 RT helix-loop-helix transcription factor";
 RL Genes Dev. 9:1009-1019(1995).
 CC -1- FUNCTION: ACTS AS A DIFFERENTIATION FACTOR DURING NEUROGENESIS.
 CC -1- TRANSCRIPTIONAL ACTIVATOR. BINDS TO THE INSULIN GENE E-BOX.
 CC -1- SUBUNIT: EFFICIENT DNA BINDING REQUIRES DIMERIZATION WITH ANOTHER
 CC BHLH PROTEIN. HETERODIMER WITH E47.
 CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).
 CC -1- TISSUE SPECIFICITY: MOST ABUNDANT IN PANCREATIC ALPHA- AND BETA-
 CC CELLS. LESS IN BRAIN AND TESTIS.
 CC -1- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
 CC TRANSCRIPTION FACTORS. "ATONAL" SUBFAMILY.

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DR EMBL: U24679; AAA8518.1; ALT INIT.
DR InterPro: IPR001092; HLH_basic.
DR Pfam: PF00010; HLH_1.
DR SMART; SM00353; HLH_1.
DR PROSITE; PS00038; HLH_1; 1.
DR PROSITE; PS00888; HLH_2; 1.
DR DNA-binding; Nuclear protein; Transcription regulation; Activator;
KW Neurogenesis; Developmental protein; Differentiation.
FT DOMAIN 58 77
FT DNA_BIND 86 92 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT DOMAIN 101 112 BASIC DOMAIN.
FT DOMAIN 113 153 HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).
FT DOMAIN 67 75 POLY-GLU.
FT DOMAIN 86 89 POLY-LYS.
SQ SEQUENCE 355 AA; 39763 MW; F4344DFD360226B2 CRC64;

Query Match
Best Local Similarity 42.1%; Pred. No. 23;
Matches 8; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 12 KXEEAVRLXXXXLKNKG 30
DB 39 KEDELEAMNAEDSLRNGG 57

RESULT 15
NDFL_MOUSE STANDARD; PRT; 357 AA.
ID NDFL_MOUSE Q60867;
AC Q60867; Q60897;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neurogenic differentiation factor 1 (Neurod1).
GN NEUROD1 OR NEUROD.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WF1 and 129/Sv;
RX MEDLINE=95273957; PubMed=7754368;
RA Lee J.E., Hollenberg S.W., Snider L., Turner D.L., Lipnick N.,
RA Weintraub H.;
RT "Conversion of Xenopus ectoderm into neurons by Neurod, a basic
RT helix-loop-helix protein."
RL Science 268:836-844(1995).
CC - FUNCTION: ACTS AS A DIFFERENTIATION FACTOR DURING NEUROGENESIS.
CC - TRANSCRIPTIONAL ACTIVATOR. BINDS TO THE INSULIN GENE E-BOX.
CC - SUBUNIT: EFFICIENT DNA BINDING REQUIRES DIMERIZATION WITH ANOTHER
CC BHLH PROTEIN. HETERODIMER WITH E47.
CC - SUBCELLULAR LOCATION: Nuclear (Potential).
CC - TISSUE SPECIFICITY: EXPRESSED IN DIFFERENTIATING NEURONS OF
CC BOTH THE CENTRAL AND PERIPHERAL NERVOUS SYSTEMS.
CC - DEVELOPMENTAL STAGE: EXPRESSED DURING EMBRYONIC DEVELOPMENT.
CC - SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
CC TRANSCRIPTION FACTORS. "ATONAL" SUBFAMILY.
CC
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CC
DR EMBL: U28068; AAC52203.1; -
DR EMBL: U28888; AAC52204.1; -
DR PIR: I49338; I49338.
DR MGI: MGI:1339708; Neurod1.
DR GO: GO:0001654; P-eye morphogenesis; IMP.
DR InterPro: IPR001092; HLH_basic.
DR Pfam: PF00010; HLH_1.

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DR SMART; SM00353; HLH_1.
DR PROSITE; PS00038; HLH_1; 1.
DR PROSITE; PS00888; HLH_2; 1.
DR DNA-binding; Nuclear protein; Transcription regulation; Activator;
KW Neurogenesis; Developmental protein; Differentiation.
FT DOMAIN 58 77
FT DNA_BIND 87 93 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT DOMAIN 102 113 BASIC DOMAIN.
FT DOMAIN 114 154 HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).
FT DOMAIN 58 64 POLY-GLU.
FT DOMAIN 67 77 POLY-GLU.
FT DOMAIN 87 90 POLY-LYS.
SQ SEQUENCE 357 AA; 39998 MW; B626E115531027 CRC64;

Query Match
Best Local Similarity 42.1%; Pred. No. 23;
Matches 8; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 12 KXEEAVRLXXXXLKNKG 30
DB 39 KEDELEAMNAEDSLRNGG 57

RESULT 16
NDFL_RAT STANDARD; PRT; 357 AA.
ID NDFL_RAT Q64289;
AC Q64289;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neurogenic differentiation factor 1 (Neurod1) (Basic helix-loop-helix
DE factor 1) (BHLH-1).
GN NEUROD1 OR NEUROD.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cerebellum;
RX MEDLINE=96220182; PubMed=8660336;
RA Kawakami H., Matuyama H., Yasunami M., Ohkubo H., Hara H., Saida T.,
RA Nakanishi S., Nakamura S.;
RT "Cloning and expression of a rat brain basic helix-loop-helix
RT factor."
RL Biochem. Biophys. Res. Commun. 221:199-204(1996).
RN [2]
RP SEQUENCE OF 88-200 FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Retina;
RA Ahmad I., Achary H.R.;
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
CC - FUNCTION: ACTS AS A DIFFERENTIATION FACTOR DURING NEUROGENESIS.
CC TRANSCRIPTIONAL ACTIVATOR. BINDS TO THE INSULIN GENE E-BOX.
CC - SUBUNIT: EFFICIENT DNA BINDING REQUIRES DIMERIZATION WITH ANOTHER
CC BHLH PROTEIN. HETERODIMER WITH E47.
CC - SUBCELLULAR LOCATION: Nuclear (Potential).
CC - SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
CC TRANSCRIPTION FACTORS. "ATONAL" SUBFAMILY.
CC
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CC
DR EMBL: D82075; BA11536.1; -
DR EMBL: D82074; BA11535.1; -
DR EMBL: U80603; AAB38744.1; -
DR PIR: JC4703; JC4703.
DR InterPro: IPR001092; HLH_basic.
DR Pfam: PF00010; HLH_1.

```


DR SMART, SMO0353; HLH, 1.
 FT PROSITE; PS00038; HLH_1; 1.
 DR PROSITE; PS00888; HLH_2; 1.
 KM DNA-binding; Nuclear protein; Transcription regulation; Activator;
 KM Neogenesis; Developmental protein; Differentiation.
 FT DOMAIN 58 77
 FT DOMAIN 87 93
 FT DNA_BIND 102 113
 FT DOMAIN 114 124
 FT DOMAIN 67 76
 FT DOMAIN 87 90
 FT POLY-LYS.
 SQ SEQUENCE 357 AA; 40000 MW; F773637E64D3E99E CRC64;

Query Match 31.4%; Score 38; DB 1; Length 357;
 Best Local Similarity 42.1%; Pred. No. 23;
 Matches 8; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 12 SKXEEAVRLXXXXXNGC 30
 Db 39 KEDELEAMNAEEDSLNNGC 57

RESULT 17
 ID DNL1_ASFM2 STANDARD; PRT; 419 AA.
 AC P26813;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE DNA ligase (EC 6.5.1.1) (polydeoxyribonucleotide synthase [ATP]).
 OS African swine fever virus (isolate Malawi Lil 20/1) [ASFV].
 CC Viruses; dsDNA viruses, no RNA stage; Asfarviridae; Asfarvirus.
 NC NCBI_TaxID=10500;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92310959; Pubmed=1614852;
 RA Hammond J.M., Kerr S.M., Smith G.L., Dixon L.K.;
 RL "An African swine fever virus gene with homology to DNA ligases";
 Nucleic Acids Res. 20:2667-2671(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94292916; Pubmed=8021596;
 RA Dixon L.K., Twigg S.R.F., Baylis S.A., Vydelingum S., Bristow C.,
 RA Hammond J.M., Smith G.L.;
 RL "Nucleotide sequence of a 55 kbp region from the right end of the
 genome of a pathogenic African swine fever virus isolate (Malawi
 Lil20/1).";
 J. Gen. Virol. 75:1655-1664(1994).
 CC -1- FUNCTION: THIS PROTEIN SEALS DNA REPLICATION, DNA
 RECOMBINATION AND DNA REPAIR NICKS IN DOUBLE-STRANDED DNA.
 CC IT IS NOT ESSENTIAL FOR VIRAL REPLICATION AND RECOMBINATION.
 CC -1- CATALYTIC ACTIVITY: ATP + (deoxyribonucleotide) (N) +
 (deoxyribonucleotide) (M) = AMP + diphosphate +
 (deoxyribonucleotide) (N+M).
 CC -1- SIMILARITY: BELONGS TO THE ATP-DEPENDENT DNA LIGASE FAMILY.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X65192; CAA46310.1; -;
 DR EMBL; X71982; CAA50805.1; -;
 DR PIR; S23018; S23018.
 DR InterPro: IPR000977; DNA_ligase.
 DR Pfam; PF01068; DNA_ligase.1.
 DR PROSITE; PS00697; DNA_LIGASE_A1; 1.
 DR PROSITE; PS00333; DNA_LIGASE_A2; 1.
 DR PROSITE; PS0160; DNA_LIGASE_A3; 1.
 KM DNA repair; DNA replication; DNA recombination; Cell division; Ligase;

KM ARP-binding. 151 151 AMP (BY SIMILARITY).
 FT BINDING 151 151
 SQ SEQUENCE 419 AA; 48041 MW; DA781C64CA1B10F0 CRC64;

Query Match 31.4%; Score 38; DB 1; Length 419;
 Best Local Similarity 42.1%; Pred. No. 28;
 Matches 8; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 11 SKXEEAVRLXXXXXNGC 29
 Db 271 SYKMEDEALRLKQFIKEG 289

RESULT 18
 ID LUT1A_LYCPN STANDARD; PRT; 589 AA.
 AC O04973;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE 2-isopropylmalate synthase A (EC 2.3.3.13) (Alpha-isopropylmalate
 synthase A) (Alpha-IPM synthetase A).
 OS IpmsA.
 CC Lycopersicon pennellii (Tomato).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 CC Asteridae; Lamiales; Solanales; Solanaceae; Solanum.
 NC NCBI_TaxID=28526;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wei T., Maite D., Steffens J.C.;
 RL "Cloning of two L. pennellii 2-isopropylmalate synthase cDNA and
 their functional expression in yeast";
 Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Catalyzes the condensation of the acetyl group of
 acetyl-CoA with 3-methyl-2-oxobutanoate (2-oxoisovalerate) to form
 3-carboxy-3-hydroxy-4-methylpentanoate (2-isopropylmalate).
 CC -1- CATALYTIC ACTIVITY: Acetyl-CoA + 3-methyl-2-oxobutanoate + H(2)O =
 2-hydroxy-2-isopropylsuccinate + CoA.
 CC -1- PATHWAY: Leucine biosynthesis; first step.
 CC -1- SIMILARITY: Belongs to the alpha-IPM synthetase / homocitrate
 synthase family. LeuA 1 subfamily.
 CC -----
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 CC -----
 DR EMBL; AF004165; AAB61598.1; -;
 DR InterPro: IPR002034; AIPM/Hcit synth.
 DR InterPro: IPR000891; HMGL-like.
 DR InterPro: IPR005671; LeuA_bact.
 DR Pfam; PF00682; HMGL-like_1.
 DR TIGRfam; TIGR00973; LeuA_bact. 1
 DR PROSITE; PS00815; AIPM_HOMOCIT_SYNTH_1; 1.
 DR PROSITE; PS00816; AIPM_HOMOCIT_SYNTH_2; FALSE_NEG.
 KM Leucine biosynthesis; Transferrase.
 SQ SEQUENCE 589 AA; 64360 MW; 150E4890018BDDF CRC64;

Query Match 31.4%; Score 38; DB 1; Length 589;
 Best Local Similarity 36.0%; Pred. No. 39;
 Matches 9; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 11 SKXEEAVRLXXXXXNGXSSGA 35
 Db 40 SKISDPKVRIFDTLLRDEQSGA 64

RESULT 19

AST2_YEAST
ID AST2_YEAST STANDARD: PRT: 430 AA.
AC P39845.
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE AST2 protein.
GN AST2 OR YER101C.
OS Saccharomyces cerevisiae (Baker's Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
[1]
RP SEQUENCE FROM N.A.
RX STRAIN=S288C / AB972;
RX PubMed=9169868;
RA Araujo R., Mulligan J.T., Hennessey K.M., Yelton M.A., Allen E.,
Cheray J.M., Chung E., Duncan M., Guzman E., Hartzell G.,
Lin D., Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P.,
Smith C., Petzel F.X., Roberts D., Sehl P., Schramm S., Shogren T.,
Smith V., Taylor P., Wei Y., Botstein D., Davis R.W.;
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome V.";
RL Nature 387:78-81(1997)
-1- SIMILARITY: HIGH, TO YEAST AST1, ALSO SIMILAR TO YMR152W.

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CC
CC EMBL: U18839; AAB64656.1; -
DR PIR: S50604; S50604.
DR SGD: S0000903; AST2.
DR GO: GO:0005737; C:cytoplasm; IDA.
DR InterPro: IPR002085; Adh_zn_family.
DR Pfam: PF00107; Adh_zinc_N; I.
SQ SEQUENCE 430 AA; 48370 MW; FEEC2F2CDE894F84 CRC64;
Query Match 30.6%; Score 37; DB 1; Length 430;
Best Local Similarity 30.0%; Pred. No. 43;
Matches 9; Conservative 5; Mismatches 16; Indels 0; Gaps 0;
OY 4 GTXXXXXKQEEAVRLXXXXKNGXSS 33
DB 182 GTALNLLAQLEKQDLNTESNVLLINGTSS 211

RESULT 20
YKTL_CABEL STANDARD: PRT: 488 AA.
ID YKTL_CABEL STANDARD: PRT: 488 AA.
AC P34312.
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Hypothetical protein C07A9.1 in chromosome III precursor.
GN C07A9.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Rhabditinae; Caenorhabditis.
OX NCBI_TaxID=6239;
[1]
RP SEQUENCE FROM N.A.
RX STRAIN=Bristol N2;
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainecough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,

RA Johnston L., Jones M., Kershaw J., Kirsten J., Laister N.,
RA Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Riken L., Roopra A., Saunders D., Showkeen R.,
RA Sims M., Smaldon N., Smith A., Smith M., Sonhammer E., Staden R.,
RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
RA Waterston R., Watson A., Weinstock L., Wilkinson-Spoat J.,
RA Mohdman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RL Nature 368:32-38(1994).
-1- SIMILARITY: Contains 1 C-type lectin family domain.

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CC
CC EMBL: Z29094; CAA82340.1; -
DR PIR: S40706; S40706.
DR HSSP: P23807; 11XX.
DR WormRep: C07A9.1; CE00502.
DR InterPro: IPR002619; CX.
DR InterPro: IPR001304; Lectin_C.
DR Pfam: PF00059; lectin_c; 1.
DR ProDom: PD006744; CX; 1.
DR SMART: SM00034; CLECT; 1.
DR PROSITE: PS00615; C-TYPE_LLECTIN_1; FALSE_NEG.
DR PROSITE: PS50041; C-TYPE_LLECTIN_2; 1.
KW Hypothetical protein; Lectin; Signal.
FT SIGNAL 1 49
FT CHAIN 50 488
FT DOMAIN 224 341
FT CARBOHYD 187 187
FT CARBOHYD 237 237
FT CARBOHYD 409 409
SQ SEQUENCE 488 AA; 54717 MW; 9022691E4707814 CRC64;
Query Match 30.6%; Score 37; DB 1; Length 488;
Best Local Similarity 30.0%; Pred. No. 49;
Matches 9; Conservative 3; Mismatches 18; Indels 0; Gaps 0;
OY 5 TXXXXXKQEEAVRLXXXXKNGXSSG 34
DB 445 TEMSRSRKEKETEDSINXSLKEGTARG 474

RESULT 21
KPBL_RABIT STANDARD: PRT: 1237 AA.
ID KPBL_RABIT STANDARD: PRT: 1237 AA.
AC P18688.
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Phosphorylase B kinase alpha regulatory chain, skeletal muscle
DE isoform (Phosphorylase kinase alpha subunit).
GN PHKA1.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
[1]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND PARTIAL SEQUENCE.
RX TISSUE=skeletal muscle;
RX MEDLINE=88203614; PubMed=3362857;
RA Zander N.F., Meyer H.E., Hoffmann-Pozorske E., Crabb J.W.,
Heilmeyer L.M.G. Jr., Killmann M.W.;
RT "cDNA cloning and complete primary structure of skeletal muscle
RT phosphorylase kinase (alpha subunit).";
RL Proc. Natl. Acad. Sci. U.S.A. 85:2929-2933(1988).

RN (2)
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 3).
 RX MEDLINE=91340693; PubMed=1874721;
 RA Harmann B., Zander N.F., Kiliann M.W.;
 RT "Isoform diversity of phosphorolase kinase alpha and beta subunits
 RT generated by alternative RNA splicing.";
 RL J. Biol. Chem. 266:15631-15637(1991).
 RN [3]
 RP SEQUENCE OF 1016-1027.
 RX MEDLINE=75130982; PubMed=164350;
 RA Cohen P., Watson D.C., Dixon G.H.;
 RT "The hormonal control of activity of skeletal muscle phosphorylase
 RT kinase. Amino-acid sequences at the two sites of action of adenosine-
 RT 3',5'-monophosphate-dependent protein kinase.";
 RL Eur. J. Biochem. 51:79-92(1975).
 RN [4]
 RP ALTERNATIVE SPLICING (ISOFORMS 1 AND 2).
 RX MEDLINE=94043107; PubMed=8226841;
 RA Muellerich A., Hamacher C., Schneider A., Kiliann M.W.;
 RT "The multiphosphorylation domain of the phosphorylase kinase alpha M
 RT and alpha L subunits is a hotspot of differential mRNA processing and
 RT of molecular evolution.";
 RL J. Biol. Chem. 268:23208-23214(1993).
 RN [5]
 RP PHOSPHORYLATION.
 RX MEDLINE=90201066; PubMed=2108025;
 RA Meyer H.E., Meyer G.F., Dirks H., Heilmeyer L.M.G. Jr.;
 RT "Localization of phosphoserine residues in the alpha subunit of
 RT rabbit skeletal muscle phosphorylase kinase.";
 RL Eur. J. Biochem. 188:357-376(1990).
 CC -1- FUNCTION IN CERTAIN SUBSTRATES, INCLUDING TROPONIN I, THE ALPHA
 CC CHAIN MAY BIND CALMODULIN.
 CC -1- ENZYME REGULATION: BY PHOSPHORYLATION OF VARIOUS SERINE RESIDUES
 CC AND BY CALCIUM.
 CC -1- PATHWAY: Glycogen metabolism.
 CC -1- SUBUNIT: POLYMER OF 16 CHAINS, FOUR EACH OF ALPHA, BETA, GAMMA,
 CC AND DELTA. ALPHA AND BETA ARE REGULATORY CHAINS, GAMMA IS THE
 CC CATALYTIC CHAIN AND DELTA IS CALMODULIN.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=1; Synonyms=ABC, Alpha;
 CC IsoId=PI8688-1; Sequence=Displayed;
 CC Name=2; Synonyms=BC;
 CC IsoId=PI8688-2; Sequence=VSP_004701;
 CC Name=3; Synonyms=Alpha';
 CC IsoId=PI8688-3; Sequence=VSP_004699, VSP_004700;
 CC -1- TISSUE SPECIFICITY: Isoform 1 predominates in muscle, heart, brain
 CC and testis. Isoforms 1 and 2 are expressed in similar quantities
 CC in the other tissues. Isoform 3 is highly expressed in slow muscle
 CC and heart.
 CC -1- PTM: THE PHOSPHORYLATION OF SERINE 1018 BY PKA STIMULATES THE
 CC DEPHOSPHORYLATION OF THE BETA SUBUNIT AND, THIS, REVERSES THE
 CC INITIAL STIMULATION OF PKA BY THE PASTER BETA SUBUNIT
 CC PHOSPHORYLATION THROUGH PKA THAT OCCURS IN MUSCLE IN RESPONSE TO
 CC ADRENALIN.
 CC -1- SIMILARITY: BELONGS TO THE PHOSPHORYLASE B KINASE REGULATORY
 CC CHAIN FAMILY.
 CC -----
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 CC -----
 DR EMBL: J03247; AAA31446.1; ALT_SEQ.
 DR EMBL: M64656; AAC23909.1; -.
 DR PIR: A31334; A31334.
 KW Glycogen metabolism; Muscle; Phosphorylation; Calmodulin-binding;
 KW Alternative splicing; Multigene family.
 FT DOMAIN 810 840 CALMODULIN-BINDING (POTENTIAL).

FT DOMAIN 1060 1100 CALMODULIN-BINDING (POTENTIAL).
 FT MOD_RES 972 972 PHOSPHORYLATION (AUTO-).
 FT MOD_RES 985 985 PHOSPHORYLATION (AUTO-).
 FT MOD_RES 1007 1007 PHOSPHORYLATION (AUTO-).
 FT MOD_RES 1018 1018 PHOSPHORYLATION (BY PKA).
 FT MOD_RES 1020 1020 PHOSPHORYLATION (PARTIAL).
 FT MOD_RES 1023 1023 PHOSPHORYLATION (PARTIAL).
 FT MOD_RES 1030 1030 PHOSPHORYLATION.
 FT MOD_RES 654 712 Missing (in isoform 3).
 FT VARSPPLIC 713 713 /Frid=VSP_004699.
 FT VARSPPLIC 713 713 N -> D (in isoform 3).
 FT VARSPPLIC 1012 1024 /Frid=VSP_004700.
 FT VARSPPLIC 1012 1024 Missing (in isoform 2).
 FT SEQUENCE 1237 AA; 138413 MW; 98535BA29D4B33FF CRC64;
 SQ
 QY Query Match 30.6%; Score 37; DB 1; Length 1237;
 DB Best Local Similarity 37.5%; Pred. No. 1.3e+02;
 DB Matches 9; Conservative 2; Mismatches 13; Indels 0; Gaps 0;
 DB 12 KYHEBAVRLXXXXLKNCGSSGA 35
 DB 1010 KYVEFRRLSTSTSGPQSGHSLGA 1033
 RESULT 22
 ID_KP2_CANAL STANDARD: PRT; 946 AA.
 AC 084200;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE 6-phosphofructokinase beta subunit (EC 2.7.1.11) (phosphofructokinase
 DE 2) (phosphohexokinase) (6P-F-1-K beta subunit) (CaPKK2).
 GN PKK2.
 OS Candida albicans (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
 ON NCBI_TaxId=5476;
 RX [1]
 RP SEQUENCE FROM N.A. AND CHARACTERIZATION.
 RC STRAIN=ATCC 10231.
 RX MEDLINE=99191702; PubMed=10091602;
 RA Loberger A., Kitchath L., Ernst J.F., Heinisch J.J.;
 RT "Genetic and biochemical characterization of phosphofructokinase from
 RT the opportunistic pathogenic yeast Candida albicans.";
 RL Eur. J. Biochem. 260:217-226(1999).
 CC -1- CATALYTIC ACTIVITY: ATP + D-fructose 6-phosphate = ADP + D-
 CC fructose 1,6-bisphosphate.
 CC -1- ENZYME REGULATION: Allosterically inhibited by ATP and activated
 CC by AMP and fructose 2,6-bisphosphate.
 CC -1- PATHWAY: Key control step of glycolysis.
 CC -1- SUBUNIT: Heterooctamer of 4 alpha and 4 beta chains (By
 CC similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: Belongs to the phosphofructokinase family. Two domains
 CC subfamily.
 CC -----
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 CC -----
 DR EMBL: AJ007637; CAB38867.1; -.
 DR HSSP: P00512; 3PFK.
 DR InterPro: IPR000023; Pfufckinase.
 DR Pfam: PF00365; PFK; 2.
 DR PRINTS: PR00476; PHFCKTKINASE.
 DR ProDom: PD000707; Pfkfrckinase; 2.
 DR PROSITE: PS00433; PHOSPHOFRUCTOKINASE; 2.

KW Kinase; Transferase; Glycolysis; Repeat; Allosteric enzyme.
SQ SEQUENCE 946 AA; 104045 MW; AEF6167A741D8672 CRC64;

Query Match 30.2%; Score 36.5; DB 1; Length 946;
Best Local Similarity 40.0%; Pred. No. 1, 2e+02;
Matches 10; Conservative 4; Mismatches 10; Indels 1; Gaps 1;

QY 11 SKOXEE-EAVRLXXXXLXNGXSSG 34
172 SRNIETKAVRRRIAVMTSGDSOG 196

RESULT 23
NSR LACLA STANDARD; PRT; 318 AA.
AC P23648;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 01-NOV-1991 (Rel. 20, Last annotation update)
DE Nisin-resistance protein.
GN NSR.
OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OX NCBI_TaxID=1360;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Biovar diacetylactis DRC3;
RX MEDLINE=91247826; PubMed=1903915;
RA Froese B.R., McKay L.L.;
RT "molecular characterization of the nisin resistance region of Lactococcus lactis subsp. lactis biovar diacetylactis DRC3.";
RL Appl. Environ. Microbiol. 57:804-811 (1991).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
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CC
CC EMBL; M37002; AAA25202.1; -;
DR PIR; A43746; A43746.
DR InterPro; IPR003581; TSPC.
DR SMART; SM00245; TSPC; 1.
KM Antibiotic resistance; Transmembrane.
FT TRANSMEM 7 28 POTENTIAL.
SQ SEQUENCE 318 AA; 35033 MW; CBF6060250C21E48 CRC64;

Query Match 29.8%; Score 36; DB 1; Length 318;
Best Local Similarity 26.7%; Pred. No. 48;
Matches 8; Conservative 4; Mismatches 18; Indels 0; Gaps 0;

QY 4 GTXXXXXSKOXEEAVRLXXXXLXNGXSS 33
184 GTLFTYVDKSSHSKPEVLONGEINGSGST 213

RESULT 24
FE22 HUMAN STANDARD; PRT; 320 AA.

ID FE22 HUMAN STANDARD; PRT; 320 AA.
AC Q9UW8; Q99690;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fasciculation and elongation protein zeta 2 (Zygin II).
GN FE22.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

RP SEQUENCE FROM N.A.
RC TISSUE=Adrenal gland;
RX MEDLINE=20402571; PubMed=10931946;
RA Hu R.-M., Han Z.-G., Song H.-D., Peng Y.-D., Huang Q.-H., Ren S.-X., Gu Y.-J., Huang C.-H., Li Y.-B., Jiang C.-L., Fu G., Zhang Q.-H., Xu B.-W., Dai M., Mao Y.-F., Gao G.-F., Rong R., Ye M., Zhou J., Xu S.-H., Gu J., Shi J.-X., Jin W.-R., Zhang C.-K., Wu T.-W., Huang G.-Y., Chen Z., Chen M.-D., Chen J.-L.;
RT "Gene expression profiling in the human hypothalamus-pituitary-adrenal axis and full-length cDNA cloning.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:9543-9548 (2000).
RN [2]
RP SEQUENCE OF 72-320 FROM N.A.
RA Sugita S., von Poser C., Rosahl T.W., Hata Y., Suedhof T.C.;
RT "Zigins: a family of synaptotagmin-interacting proteins related to unc-76.";
RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 168-320 FROM N.A.
RX MEDLINE=97250552; PubMed=9096408;
RA Bloom L., Horvitz H.R.;
RT "The Caenorhabditis elegans gene unc-76 and its human homologs define a new gene family involved in axonal outgrowth and fasciculation.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:3414-3419 (1997).
CC -1- FUNCTION: INVOLVED IN AXONAL OUTGROWTH AND FASCICULATION (BY SIMILARITY).
CC -1- SUBUNIT: INTERACTS WITH SYNAPTOTAGMIN.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN NONNEURAL TISSUES, SUCH AS HEART, LUNG, SPLEEN, MUSCLE, TESTIS, PLACENTA, AND MELANOCYTES.
CC -1- SIMILARITY: BELONGS TO THE ZYGIN FAMILY.

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CC
CC EMBL; AF113124; AF11865.1; -;
DR EMBL; U69140; AAB40661.1; -;
DR EMBL; U60061; AAC51283.1; -;
DR Genew; HGNC:3660; FE22.
DR MTM; 604826; -;
DR GO; GO:0007411; P:axon guidance; TAS.
DR GO; GO:0007399; P:neurogenesis; TAS.
DR GO; GO:0007165; P:signal transduction; TAS.
KM Coiled coil.
FT DOMAIN 179 252 COILED COIL (POTENTIAL).
FT DOMAIN 245 251 POLY-LYS.
SQ SEQUENCE 320 AA; 36166 MW; 489CEFE0294E015 CRC64;

Query Match 29.8%; Score 36; DB 1; Length 320;
Best Local Similarity 33.3%; Pred. No. 48;
Matches 8; Conservative 3; Mismatches 13; Indels 0; Gaps 0;

QY 11 SKOXEEAVRLXXXXLXNGXSSG 34
235 NKQKHETAKKKKKLXNGSSQNG 258

RESULT 25
FE22 RAT STANDARD; PRT; 324 AA.

ID FE22 RAT STANDARD; PRT; 324 AA.
AC P97578; Q9UJ35; Q9UJ36;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fasciculation and elongation protein zeta 2 (Zygin II) (Zygin-related protein types I/II) (Fragment).
GN FE22 OR ZRP1 OR ZRP2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Sugita S., von Poser C., Rosahl T.W., Hata Y., Suedhof T.C.;
 RT "Zigons: a family of synaptotagmin-interacting proteins related to
 RT unc-46";
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 RN (2)
 RP SEQUENCE OF 246-324 FROM N.A.
 RC STRAIN=Fischer; TISSUE=Fibroblast;
 RA Zhang Q.Y., Blair D.G.;
 RT "Effective generation of viral/cell fusion transcripts by poly-A
 RT signal sequence mutant retroviruses:evidence for increased
 RT tumorigenicity by infected rat fibroblasts";
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: INVOLVED IN AXONAL OUTGROWTH AND FASCICULATION (BY
 CC SIMILARITY).
 CC -1- SUBUNIT: INTERACTS WITH SYNAPTOTAGMIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE ZYGIN FAMILY.
 CC -----
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 CC -----
 DR EMBL: U64689; AAB40631.1; -
 DR EMBL: AF120109; AAF87266.1; -
 DR EMBL: AF120110; AAF87267.1; -
 KW Coiled coil.
 FT NON TER 1 1
 FT DOMAIN 105 126 COILED COIL (POTENTIAL).
 FT DOMAIN 154 229 COILED COIL (POTENTIAL).
 SQ SEQUENCE 324 AA; 36628 MW; 21B6C6AD9562A6A7 CRC64;
 QY Query Match 29.8%; Score 36; DB 1; Length 324;
 Best Local Similarity 33.3%; Pred. No. 49;
 Matches 8; Conservative 3; Mismatches 13; Indels 0; Gaps 0;
 OY 11 SKXEEAVRLXXXXLKNKGXSSG 34
 DB 212 NKOKEKETAKKKKKLKNKGSSONG 235
 RESULT 26
 ID GLXA RHIME STANDARD; PRT; 324 AA.
 AC 087389;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Transcriptional regulator GLXA.
 GN GLXA OR R00086 OR SMC02609.
 OS Rhizobium meliloti (Sinorhizobium meliloti).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
 OX NCBI_TaxID=382;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=1021;
 RA Powers E.L., Vuyyuru V., Kahn M.L.;
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 RN (2)
 RP SEQUENCE FROM N.A.
 RC STRAIN=1021;
 RA Capela D., Balloy-Hudler F., Gouzy J., Bothe G., Ampe F., Batur J.,
 RA Bolstead P., Becker A., Boutry M., Cadieu S., Dreano S., Gloux S.,
 RA Godard T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masny D.,
 RA Pohl T., Portetelle D., Puhler A., Purnelle B., Rameperger U.,

RA Renard C., Thebaud P., Vandenbol M., Weiner S., Gallibert F.;
 RT "Analysis of the chromosome sequence of the legume symbiont
 RT Sinorhizobium meliloti strain 1021";
 RL Proc. Natl. Acad. Sci. U.S.A. 96:9877-9882(2001).
 CC -1- SIMILARITY: BELONGS TO THE ARAC/XYS FAMILY OF TRANSCRIPTIONAL
 CC REGULATORS.
 CC -----
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 CC -----
 DR EMBL: AF055582; AAC62219.1; -
 DR EMBL: AL591782; CAC41473.1; -
 DR InterPro: IPR000005; HTHARAC.
 DR InterPro: IPR002818; TH1J
 DR Pfam: PF01965; D1-PfD1.1.
 DR Pfam: PF00165; HTH_Arac.2.
 DR PRINTS: PR00032; HTHARAC.
 DR SMART: SM00342; HTH_ARAC.1.
 DR PROSITE: PS00041; HTH_ARAC_FAMILY_1; 1.
 DR PROSITE: PS01124; HTH_ARAC_FAMILY_2; 1.
 KW Transcription regulation; DNA-binding; Complete proteome.
 FT DNA_BIND 239 257 H-T-H MOTIF (BY SIMILARITY).
 SQ SEQUENCE 324 AA; 34959 MW; 4D622F54J3575D0D CRC64;
 QY Query Match 29.8%; Score 36; DB 1; Length 324;
 Best Local Similarity 50.0%; Pred. No. 49;
 Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
 OY 20 RLXXXXLKNKGXSSGA 35
 DB 103 RLRLGIRIGISSGA 118
 RESULT 27
 ID VP35 VACCC STANDARD; PRT; 324 AA.
 AC P20497;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Immunodominant envelope protein p35 (Viroion envelope protein p35).
 GN H3L.
 OS Vaccinia virus (strain Copenhagen).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 OX NCBI_TaxID=10249;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91021027; PubMed=2219722;
 RA Goebel S.J., Johnson G.P., Perkins M.E., Davis S.W., Winslow J.P.,
 RA Paolletti E.;
 RL "The complete DNA sequence of vaccinia virus";
 RL Virology 179:247-266(1990).
 RN (2)
 RP COMPLETE GENOME.
 RA Goebel S.J., Johnson G.P., Perkins M.E., Davis S.W., Winslow J.P.,
 RA Paolletti E.;
 RL "Appendix to 'The complete DNA sequence of vaccinia virus'";
 RL Virology 179:517-563(1990).
 CC -----
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 CC -----

DR EMBL; M35027; AAA48090.1; -
 DR PIR; C42514; C42514.
 DR InterPro; IPR004900; Pox_P35.
 DR Pfam; PF03213; Pox_P35; 1.
 KW Envelope protein; Late protein.
 SQ SEQUENCE 324 AA; 37458 MW; ED326A2B3875EB32 CRC64;

Query Match 29.8%; Score 36; DB 1; Length 324;
 Best Local Similarity 41.2%; Pred. No. 49;
 Matches 7; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 18 AVRLXXXXLKNKGXSSG 34
 | : : : : :
 DB 195 ALNIVDEIKSGGLSSG 211

RESULT 28
 VP35 VARV STANDARD; PRT; 325 AA.
 AC P33059;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Immunodominant envelope protein p35 (Varion envelope protein p35).
 GN H3L OR 13L.
 OS Variola virus.
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 OX NCBI_TaxID=10255;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=India-1967 / Isolate Ind3;
 RX MEDLINE=93190624; PubMed=8383392;
 RA Shchelkunov S.N., Blinov V.M., Totmenin A.V., Marenikova S.S.,
 RA Kolychalov A.A., Frolov I.V., Chizhikov V.E., Gyrolov V.V.,
 RA Gashnikov P.V., Belanov E.F., Belavin P.A., Resenchuk S.M.,
 RA Andzhaparidze O.G., Sandakhchiev L.S.,
 RT "Nucleotide sequence analysis of variola virus HindIII M, L, I genome
 RT fragments";
 RL Virus Res. 27:25-35 (1993).
 RN [2]
 RP COMPLETE GENOME.
 RC STRAIN=India-1967 / Isolate Ind3;
 RX MEDLINE=9320281; PubMed=8384129;
 RA Shchelkunov S.N., Blinov V.M., Sandakhchiev L.S.,
 RT "Genes of variola and vaccinia viruses necessary to overcome the host
 RT protective mechanisms";
 RL FEBS Lett. 319:80-83 (1993).
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DR EMBL; X67119; CAA7585.1; -
 DR EMBL; S55844; AAB24682.1; -
 DR EMBL; X69198; CAA49027.1; -
 DR PIR; S33100; S33100.
 DR InterPro; IPR004900; Pox_P35.
 DR Pfam; PF03213; Pox_P35; 1.
 KW Envelope protein; Late protein.
 SQ SEQUENCE 325 AA; 37695 MW; EAB2FE3CDEA6E40 CRC64;

Query Match 29.8%; Score 36; DB 1; Length 325;
 Best Local Similarity 41.2%; Pred. No. 49;
 Matches 7; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 18 AVRLXXXXLKNKGXSSG 34
 | : : : : :
 DB 196 ALNIVDEIKSGGLSSG 212

RESULT 29
 BIOF_AQUAE STANDARD; PRT; 373 AA.
 ID BIOF_AQUAE
 AC O66875;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE 8-amino-7-oxononanoate synthase (EC 2.3.1.47) (AONS) (8-amino-7-
 DE ketopelargonate synthase) (7-keto-8-amino-pelargonic acid synthetase)
 DE (7-KAP synthetase) (L-alanine--pimelyl CoA lyase).
 GN BIOF OR AQ 626.
 OS Aquifex aeolicus.
 OC Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
 OX NCBI_TaxID=63363;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VFS;
 RX MEDLINE=98196666; PubMed=9537320;
 RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
 RA Graham D.E., Overbeek R., Sneed M.A., Keller M., Anjaly M., Huber R.,
 RA Feldman R.A., Short J.M., Olson G.J., Sanson R.V.;
 RT "The complete genome of the hyperthermophilic bacterium Aquifex
 RT aeolicus";
 RL Nature 392:353-358 (1998).
 CC -1- CATALYTIC ACTIVITY: 6-carboxyhexanoyl-CoA + L-alanine = 8-amino-7-
 CC oxononanoate + CoA + CO(2).
 CC -1- COFACTOR: Pyridoxal phosphate (By similarity).
 CC -1- PATHWAY: Biotin biosynthesis; first step.
 CC -1- SIMILARITY: BELONGS TO CLASS-II OF PYRIDOXAL-PHOSPHATE-DEPENDENT
 CC AMINOTRANSFERASES.
 CC
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DR EMBL; AE000699; AAC06836.1; -
 DR PIR; G70355; G70355.
 DR HSSP; P12988; 1BS0.
 DR InterPro; IPR003408; Ala_synthase.
 DR InterPro; IPR004839; Aminotransferase/2.
 DR InterPro; IPR004723; BioF.
 DR InterPro; IPR001917; Nitransf_2.
 DR Pfam; PF02490; Ala_synthase; 1.
 DR Pfam; PF00155; aminotran_1_2; 1.
 DR TIGRFAMs; TIGR00658; bioF; 1.
 DR PROSITE; PS00599; AA_TRANSFER_CLASS_2; 1.
 KW Biotin biosynthesis; Transferase; Pyridoxal phosphate;
 KW Complete proteome.
 FT BINDING 223
 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
 SQ SEQUENCE 373 AA; 42532 MW; 536B34A5DF84401 CRC64;

Query Match 29.8%; Score 36; DB 1; Length 373;
 Best Local Similarity 45.0%; Pred. No. 56;
 Matches 9; Conservative 3; Mismatches 4; Indels 4; Gaps 1;

OY 16 EAVALXXXXLKNKGXSSG 35
 | : : : : :
 DB 45 ESIRV---LKEAGLSSG 60

RESULT 30
 CPXP_BRAJA STANDARD; PRT; 401 AA.
 ID CPXP_BRAJA
 AC Q59203;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)

```

DE Cytochrome P450 B7-1 (EC 1.14.14.-) (Cytochrome P450 112).
GN CYP112 OR BIR2144
OS Bradyrhizobium japonicum.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Bradyrhizobium.
OX NCBI_TaxID=375;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=USDA 110;
RA Tully R.E., Keister D.L.;
RT "Cloning and mutagenesis of a cytochrome P-450 locus from
RT Bradyrhizobium japonicum that is expressed anaerobically and
RT symbiotically."
RL Appl. Environ. Microbiol. 59:4136-4142(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=USDA 110;
RX MEDLINE=98322110; PubMed=9655913;
RA Tully R.E., van Berkum P., Lovins K.W., Keister D.L.;
RT "Identification and sequencing of a cytochrome P450 gene cluster from
RT Bradyrhizobium japonicum."
RL Biochim. Biophys. Acta 1398:243-255(1998).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=USDA 110;
RX MEDLINE=22464998; PubMed=12597275;
RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiyama T.,
RA Sasamoto S., Watanabe A., Idesawa K., Iritsugu M., Kawashima K.,
RA Kohara M., Matsumoto M., Shimo S., Tsuruoka H., Wada T., Yamada M.,
RA Tabata S.;
RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
RT Bradyrhizobium japonicum USDA110."
RL DNA Res. 9:189-197(2002).
CC -1- FUNCTION: CYTOCHROMES P450 ARE A GROUP OF HEME-THIOLATE
CC MONOOXYGENASES. THEY OXIDIZE A VARIETY OF STRUCTURALLY UNRELATED
CC COMPOUNDS, INCLUDING STEROIDS, FATTY ACIDS, AND XENOBIOTICS.
CC -1- SIMILARITY: Belongs to the cytochrome P450 family.
CC -----
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CC -----
DR EMBL: U12678; AAC28889.1; -.
DR EMBL: AP005942; BAC47409.1; -.
DR F01: 140208; 140208.
DR HSSP: Q00441; 10XA.
DR InterPro: IPR001128; Cytochrome_P450.
DR Pfam: PF00067; P450; 1.
DR PRINTS: PR00385; P450.
DR PROSITE: PS00086; CYTOCHROME_P450; 1.
KW Oxidoreductase; Monooxygenase; Electron transport; Heme;
KW Complete proteome.
FT METAL 350 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT CONFLICT 251 L -> H (IN REF. 1 AND 2).
FT CONFLICT 275 E -> Q (IN REF. 1 AND 2).
SQ SEQUENCE 401 AA; 44473 MW; 41DF690D11FDD45A CRC64;

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Query Match          29.8%; Score 36; DB 1; Length 401;
Best Local Similarity 45.8%; Pred. No. 61;
Matches 11; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

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QY 12 KXEEAVLXXXXLNGXSSGA 35
DB 221 KASEEAVGLAAGMLVAGHSTVA 244

```

Search completed: December 23, 2003, 10:01:58
Job time : 12 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 23, 2003, 09:59:56 ; Search time 28.5 Seconds

(without alignments)
362.179 Million cell updates/sec

Title: US-09-889-331A-47
Sequence: 1 XXXGTXXXXXKQXEEAVRLXXXXLKXGSGSGAXXXX 40

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seque, 258052604 residues
Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database :
1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP invertebrate:*
6: SP mammal:*
7: SP mhc:*
8: SP organelle:*
9: SP phage:*
10: SP plant:*
11: SP rodent:*
12: SP virus:*
13: SP vertebrate:*
14: SP unclassified:*
15: SP rvirus:*
16: SP bacteriophage:*
17: SP archaea:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	36.4	785	12	P89451
2	42	34.7	310	16	Q9C1F8
3	42	34.7	546	16	Q8ZQW9
4	42	34.7	546	16	Q8ZQW9
5	42	34.7	546	16	Q8ZQW9
6	42	34.7	546	16	Q8ZQW9
7	41	33.9	157	16	Q9HJ00
8	41	33.9	167	16	Q9HJ00
9	41	33.9	306	12	Q9A5D9
10	41	33.9	402	17	Q9JY76
11	41	33.9	589	4	Q96L69
12	41	33.9	589	11	Q8C7V2
13	41	33.9	589	11	Q8BRG4
14	41	33.9	2052	5	Q9VFN8
15	41	33.9	2061	5	Q8MT93
16	41	33.9	2072	5	Q9VFN7

17	41	33.9	2918	16	Q8P9Q5	Q8P9Q5 xanthomonas
18	41	33.9	4753	16	Q8PL13	Q8PL13 xanthomonas
19	40	33.1	127	16	P96631	P96631 bacillus su
20	40	33.1	374	5	Q9U184	Q9U184 leishmania
21	40	33.1	455	10	Q9LHL3	Q9LHL3 arabidopsis
22	40	33.1	567	5	Q9GNX7	Q9GNX7 leishmania
23	40	33.1	609	10	Q9SD72	Q9SD72 arabidopsis
24	40	33.1	772	10	Q9SN69	Q9SN69 arabidopsis
25	40	33.1	773	5	Q8T919	Q8T919 drosophila
26	40	33.1	773	5	Q9VZK7	Q9VZK7 drosophila
27	40	33.1	1296	2	Q9KX3	Q9KX3 mycoplasma
28	40	33.1	2382	2	Q9NKP4	Q9NKP4 leishmania
29	39	32.2	145	2	P70746	P70746 aeromonas h
30	39	32.2	208	17	Q58594	Q58594 pseudomonas
31	39	32.2	342	2	Q923U2	Q923U2 pseudomonas
32	39	32.2	342	2	Q9R2T7	Q9R2T7 pseudomonas
33	39	32.2	342	2	Q9R733	Q9R733 pseudomonas
34	39	32.2	343	2	Q1180	Q1180 pseudomonas
35	39	32.2	580	16	Q988F6	Q988F6 rhizobium 1
36	39	32.2	644	10	Q8W429	Q8W429 oryza sativ
37	39	32.2	688	16	Q25812	Q25812 helicobacte
38	39	32.2	688	16	Q9ZK11	Q9ZK11 helicobacte
39	39	32.2	784	10	Q8L425	Q8L425 oryza sativ
40	39	32.2	1050	17	Q8PU41	Q8PU41 methanosarc
41	39	32.2	1649	16	Q9CFA2	Q9CFA2 lactococcus
42	38.5	31.8	472	16	Q9KX2	Q9KX2 streptomyce
43	38.5	31.8	523	10	Q8LMQ9	Q8LMQ9 oryza sativ
44	38.5	31.8	653	10	Q41729	Q41729 zea mays (m
45	38.5	31.8	1702	11	Q54875	Q54875 ratius norv
46	38	31.4	214	12	Q9PZU6	Q9PZU6 hepatitis d
47	38	31.4	239	10	Q9LTV4	Q9LTV4 arabidopsis
48	38	31.4	241	5	Q64317	Q64317 scapomyza
49	38	31.4	241	5	Q99183	Q99183 scapomyza
50	38	31.4	274	16	Q8UDB8	Q8UDB8 agrobacteri

ALIGNMENTS

RESULT 1
P89451 PRELIMINARY; PRT; 785 AA.
ID P89451;
AC P89451;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE UL28 protein.
GN UL28.
OS Herpes simplex virus (type 2).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=10310;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HG52;
RC MEDLINE=87111457; PubMed=3027242;
RX McGeech D.J., Moss H.W., McNab D., Frame M.C.;
RT "DNA sequence and genetic content of the HindIII 1 region in the short
RT unique component of the herpes simplex virus type 2 genome:
RT identification of the gene encoding glycoprotein G, and evolutionary
RT comparisons.",
RL J. Gen. Virol. 68:19-38 (1987).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=HG52;
RC MEDLINE=90278430; PubMed=2161906;
RX Everett R., Fenwick M.;
RT "Comparative DNA sequence analysis of the host shut-off genes of
RT different strains of herpes simplex virus: type 2 strain HG52 encodes
RT a truncated UL41 product.",
RL J. Gen. Virol. 71:1387-1390 (1990).
RN [3]
RP SEQUENCE FROM N.A.

RC STRAIN=HG52;
 RX MEDLINE=92113549; PubMed=162697;
 RA McGeoch D.J., Cunningham C., McIntyre G., Dolan A.;
 RT "Comparative sequence analysis of the long repeat regions and
 RT adjoining parts of the long unique regions in the genomes of herpes
 RT simplex viruses types 1 and 2.";
 RL J. Gen. Virol. 72:3057-3075 (1991).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HG52;
 RX MEDLINE=92356101; PubMed=1322965;
 RA Barnett B.C., Dolan A., Telford E.A.R., Davison A.J., McGeoch D.J.;
 RT "A novel herpes simplex virus gene (UL49) encodes a putative membrane
 RT protein with counterparts in other herpesviruses.";
 RL J. Gen. Virol. 73:2167-2171 (1992).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HG52;
 RA Dolan A.;
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Z86099; CAB06753.1; -;
 DR InterPro; IPR00501; Proc_transpt.
 DR Pfam; PF01366; PRT; 1.
 SQ SEQUENCE 785 AA; 85240 MW; 246988E41997DF62 CRC64;

Query Match 36.4%; Score 44; DB 12; Length 785;
 Best Local Similarity 41.7%; Pred. No. 23;
 Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 12 KXEEBAVRLXXXXKNGXSSGA 35
 Db 422 EQCDEALRVRLAGAGATGGA 445

RESULT 2
 09C1F8 PRELIMINARY; PRT; 310 AA.
 AC 09C1F8;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Mevalonate kinase.
 GN YKAG OR IL0404.
 OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
 OX NCBI_TaxID=1360;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=IL1403;
 RX MEDLINE=21235186; PubMed=11337471;
 RA Bojotin A., Wincker P., Manger S., Tallon O., Malame K.,
 RA Weissenbach J., Ehrlich S.D., Sorokin A.;
 RT "The complete genome sequence of the lactic acid bacterium Lactococcus
 RT lactis ssp. lactis IL1403.";
 RL Genome Res. 11:731-753 (2001).
 DR EMBL; AE006277; AAK04502.1; -;
 DR InterPro; IPR006204; GMP_kinase.
 DR InterPro; IPR006205; MvGalk_kinase.
 DR Pfam; PF00268; GMP_kinase; 1.
 DR PRINTS; PR00359; MEYGALKINASE.
 DR KINASE; Complete proteome.
 SQ SEQUENCE 310 AA; 34334 MW; E85A2C962C943BDA CRC64;

Query Match 34.7%; Score 42; DB 16; Length 310;
 Best Local Similarity 33.3%; Pred. No. 20;
 Matches 7; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 13 QXEEBAVRLXXXXKNGXSS 33
 Db 285 ENEXDAIRISQRLKNGAKRT 305

RESULT 3

Q8ZQM9 PRELIMINARY; PRT; 546 AA.
 AC Q8ZQM9;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Phosphoglucosyltransferase (EC 5.4.2.2).
 GN PGM OR STM0699.
 OS Salmonella typhimurium.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Salmonella.
 OX NCBI_TaxID=602;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
 RX MEDLINE=21534948; PubMed=11677609;
 RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
 RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
 RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Milvanev E.,
 RA Ryan E., Sun H., Flores L., Miller W., Stoneking T., Nhan M.,
 RA Waterston R., Wilson R.K.;
 RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
 RT LT2.";
 RL Nature 413:852-856 (2001).
 DR EMBL; AE008728; AAL19642.1; -;
 DR InterPro; IPR005841; PG/PMM_mutase.
 DR InterPro; IPR005852; Polysaccharide A.
 DR InterPro; IPR005844; PG_PMM_ABAI.
 DR InterPro; IPR005845; PG_PMM_ABAII.
 DR InterPro; IPR005846; PG_PMM_ABAIII.
 DR InterPro; IPR005843; PG_PMM_C.
 DR Pfam; PF00408; PGM_PMM; 1.
 DR Pfam; PF02879; PGM_PMM_I; 1.
 DR Pfam; PF02879; PGM_PMM_II; 1.
 DR Pfam; PF02880; PGM_PMM_III; 1.
 DR TIGRfam; TIGR01132; pgm; 1.
 DR PROSITE; PS00710; PGM_PMM; 1.
 DR IsoMase; Complete proteome.
 SQ SEQUENCE 546 AA; 58089 MW; A3DD0779F6AE8C95 CRC64;

Query Match 34.7%; Score 42; DB 16; Length 546;
 Best Local Similarity 52.9%; Pred. No. 36;
 Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 12 KXEEBAVRLXXXXKXN 28
 Db 529 KOIEKAEVIVSEVLKN 545

RESULT 4
 08Z8F1 PRELIMINARY; PRT; 546 AA.
 AC 08Z8F1;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Phosphoglucosyltransferase.
 GN STY0736.
 OS Salmonella typhi.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Salmonella.
 OX NCBI_TaxID=601;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CT18;
 RX MEDLINE=21534947; PubMed=11677608;
 RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
 RA Churcher C., Mangall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
 RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
 RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
 RA Felwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jorgels K.,
 RA Krogh A., Larsen T.S., Leather S., Moule S., O'Garra P., Parry C.,
 RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,

RA Whitehead S., Barrell B.G.:
 RT "Complete genome sequence of a multiple drug resistant *Salmonella*
 RL *enterica* serovar Typhimurium CT18.";
 DR Nature 413:848-852(2001).
 DR EMBL AL627267; CAD05161.1;
 DR InterPro: IPR005841; PG_PMM_mutase.
 DR InterPro: IPR005852; Pglucmutase A.
 DR InterPro: IPR005844; PG_PMM_ABAI.
 DR InterPro: IPR005845; PG_PMM_ABAI.
 DR InterPro: IPR005846; PG_PMM_ABAI.
 DR InterPro: IPR005843; PG_PMM_C.
 DR Pfam: PF00408; FGM_PMM_1.
 DR Pfam: PF02878; FGM_PMM_II; 1.
 DR Pfam: PF02879; FGM_PMM_II; 1.
 DR Pfam: PF02880; FGM_PMM_III; 1.
 DR TIGRfams: TIGR01132; psm; 1.
 DR PROSITE: PS00710; FGM_PMM; 1.
 KM Complete proteome.
 SQ SEQUENCE 546 AA; 58127 MW; 6F73775E0B886CD8 CRC64;
 Query Match 34.7%; Score 42; DB 16; Length 546;
 Best Local Similarity 52.9%; Pred. No. 36;
 Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
 QY 12 KXEEAVRLXXXXLKN 28
 DB 529 KQLEKAEIVSEVLKN 545
 RESULT 5
 ID 08X9G6 PRELIMINARY; PRT; 546 AA.
 AC 08X9G6;
 DT 01-MAR-2002 (TReMBLrel. 20, Created)
 DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
 DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
 DE Phosphoglucmutase.
 GN PGM OR 20837 OR ECG0719.
 OS *Escherichia coli* O157:H7.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=83334;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=O157:H7 / ATCC 700927;
 RX MEDLINE=21074935; PubMed=11206551;
 RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
 RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
 RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
 RA Grodzick E.J., Davis N.W., Lim A., Dimalanta E.T., Potamocis K.,
 RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
 RA Welch R.A., Blattner F.R.;
 RT "Genome sequence of enterohaemorrhagic *Escherichia coli* O157:H7.";
 RL Nature 409:529-533(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=O157:H7 / RIMD 0509952;
 RX MEDLINE=21156231; PubMed=1158796;
 RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
 RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
 RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
 RA Kihara S., Shiba T., Harcori M., Shingawa H.;
 RT "Complete genome sequence of enterohaemorrhagic *Escherichia coli*
 RT O157:H7 and genomic comparison with a laboratory strain K-12.";
 RL DNA Res. 8:111-22(2001).
 DR EMBL AE005247; AAG55011.1;
 DR EMBL AE005252; BAB34142.1;
 DR InterPro: IPR005841; PG_PMM_mutase.
 DR InterPro: IPR005852; Pglucmutase A.
 DR InterPro: IPR005844; PG_PMM_ABAI.
 DR InterPro: IPR005845; PG_PMM_ABAI.
 DR InterPro: IPR005846; PG_PMM_ABAI.
 DR InterPro: IPR005843; PG_PMM_C.

DR Pfam: PF00408; FGM_PMM; 1.
 DR Pfam: PF02878; FGM_PMM_II; 1.
 DR Pfam: PF02879; FGM_PMM_II; 1.
 DR Pfam: PF02880; FGM_PMM_III; 1.
 DR TIGRfams: TIGR01132; psm; 1.
 DR PROSITE: PS00710; FGM_PMM; 1.
 KM Complete proteome.
 SQ SEQUENCE 546 AA; 58335 MW; 0605228081D7A31B CRC64;
 Query Match 34.7%; Score 42; DB 16; Length 546;
 Best Local Similarity 52.9%; Pred. No. 36;
 Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
 QY 12 KXEEAVRLXXXXLKN 28
 DB 529 KQLEKAEIVSEVLKN 545
 RESULT 6
 ID 08FVJ9 PRELIMINARY; PRT; 563 AA.
 AC 08FVJ9;
 DT 01-MAR-2003 (TReMBLrel. 23, Created)
 DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
 DE Phosphoglucmutase (EC 5.4.2.2).
 GN PGM OR C0775.
 OS *Escherichia coli* O6.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=217992;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=O6:H1 / CFT073 / ATCC 700928;
 RX MEDLINE=22388234; PubMed=12471157;
 RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
 RA Raeko D., Buckles E.J., Liu S.-R., Boutin A., Hackett J., Stroud D.,
 RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
 RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
 RT "Extensive mosaic structure revealed by the complete genome sequence
 RT of uropathogenic *Escherichia coli*.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
 DR EMBL AE016757; AAN79248.1;
 KM Isomerase; Complete proteome.
 SQ SEQUENCE 563 AA; 60396 MW; 3C601C329CA3B862 CRC64;
 Query Match 34.7%; Score 42; DB 16; Length 563;
 Best Local Similarity 52.9%; Pred. No. 37;
 Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
 QY 12 KXEEAVRLXXXXLKN 28
 DB 546 KQLEKAEIVSEVLKN 562
 RESULT 7
 ID 09RJTO PRELIMINARY; PRT; 157 AA.
 AC 09RJTO;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
 DE Hypothetical protein DR2500.
 GN DR2500.
 OS *Deinococcus radiodurans*.
 OC Bacteria; Deinococcus-thermus; Deinococci; Deinococcales;
 OC Deinococcaceae; Deinococcus.
 OX NCBI_TaxID=1299;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=R1;
 RX MEDLINE=20036896; PubMed=10567266;
 RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,

RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
 RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
 RA Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
 RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
 RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
 RA Fraser C.M.;
 RT "Genome sequence of the radioresistant bacterium Deinococcus
 RT radiodurans RI.";
 RL Science 286:1571-1577 (1999).
 DR EMBL; AE002079; AAF12045.1; -
 DR TIGR; DR2500; -
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 157 AA; 17027 MW; B76BD89f60A5B5D CRC64;

Query Match 33.9%; Score 41; DB 16; Length 157;
 Best Local Similarity 42.1%; Pred. No. 14;
 Matches 8; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 16 EEAVRLXXXXLNGXSSG 34
 Db 74 DDAVGFYRALNAGLDSG 92

RESULT 8

Q9ADJ9 PRELIMINARY; PRT; 167 AA.
 AC 09ADJ9:
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Putative deaminase.
 GN SC04974 OR 2SC31.34.
 OS Streptomyces coelicolor.
 OC Bacteria; Actinobacteria; Actinomycetales;
 OC Streptomycinae; Streptomycetaceae; Streptomyces.
 NCBI_TaxID=1902;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RX MEDLINE=97000351; PubMed=8843436;
 RA Redenbach M., Kieseer H.M., Denaparte D., Eichner A., Cullum J.,
 RA Kinashi H., Hopwood D.A.;
 RT "A set of ordered cosmids and a detailed genetic and physical map for
 RT the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
 RL Mol. Microbiol. 21:77-96(1996).
 RN (2)
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2) / M145;
 RX MEDLINE=21996410; PubMed=12000953;
 RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,
 RA Thomson N.R., James K.D., Harris D.E., Oball M.A., Kieseer H.,
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
 RA Huang C.-H., Kieseer T., Larke L., Murphy L., Oliver K., O'Neill S.,
 RA Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 RA Warren T., Wietzorrek A., Woodward J., Barrett B.G., Parkhill J.,
 RA Hopwood D.A.;
 RT "Complete genome sequence of the model actinomycete Streptomyces
 RT coelicolor A3(2).";
 RL Nature 417:141-147(2002).
 DR EMBL; AL939122; CAD30959.1; -
 DR InterPro; IPR002125; dCMP/cyt.deam.
 DR Pfam; PF00383; dCMP_cyt.deam.1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 167 AA; 18334 MW; 3D2044BA1FE9B1 CRC64;

Query Match 33.9%; Score 41; DB 16; Length 167;
 Best Local Similarity 35.0%; Pred. No. 15;
 Matches 7; Conservative 5; Mismatches 8; Indels 0; Gaps 0;
 Qy 16 EEAVRLXXXXLNGXSSG 35
 :||:| :||| |

Db 19 DKAIELATTSVRNGGPFCA 38

RESULT 9
 O92527 PRELIMINARY; PRT; 306 AA.
 ID 092527:
 AC 092527:
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Coat protein (capsid protein).
 OS Carnation latent virus (CLV).
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Carlavirus.
 NCBI_TaxID=12164;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Meenan B.M.;
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 RN (2)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Leaves of Dianthus barbatus;
 RX MEDLINE=91324119; PubMed=1713905;
 RA Meenan B.M., Mills P.R.;
 RT "Nucleotide sequence of the 3'-terminal region of carnation latent
 RT virus.";
 RL Intervirology 32:262-267(1991).
 CC -1- FUNCTION: SELF-ASSEMBLES WITH THE RNA TO FORM INFECTIOUS PARTICLES
 CC -1- SIMILARITY: BELONGS TO THE POTEXVIRUSES COAT PROTEIN FAMILY.
 CC (BY SIMILARITY).
 DR EMBL; AJ010697; CA009306.1; -
 DR EMBL; X52627; CA36854.1; -
 DR InterPro; IPR000052; P1vtr.coat.
 DR Pfam; PF00286; virus_P-coat.1.
 DR PRINTS; PR00232; POTXCARLCOAT.
 DR ProDom; PD000603; P1vtr.coat; 1.
 DR PROSITE; PS00418; POTEX_CARLAVIRUS_COAT; 1.
 KW Coat protein.
 SQ SEQUENCE 306 AA; 33890 MW; 4456EBB53E174298 CRC64;

Query Match 33.9%; Score 41; DB 12; Length 306;
 Best Local Similarity 43.5%; Pred. No. 30;
 Matches 10; Conservative 1; Mismatches 12; Indels 0; Gaps 0;
 Qy 12 KXEEAVRLXXXXLNGXSSG 34
 Db 62 KXKEPNSQULTAGELNGGFESG 84

RESULT 10
 Q9UYT6 PRELIMINARY; PRT; 402 AA.
 ID 09UYT6:
 AC 09UYT6:
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Molymedum cofactor biosynthesis protein (MOEA-1).
 GN PAB136.
 OS Pyrococcus abyssi.
 OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
 OC Pyrococcus.
 NCBI_TaxID=29292;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=SES / Orsay;
 RA Heilig R.;
 RT "Pyrococcus abyssi genome sequence: insights into archaeal chromosome
 RT structure and evolution.";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ248287; CAB50326.1; -
 DR InterPro; IPR001453; MoCF_biosynth.
 DR InterPro; IPR005111; MoEA_C.
 DR InterPro; IPR005110; MoEA_N.
 DR Pfam; PF00994; MoCF_biosynth; 1.

DR Pfam; PF03454; MoeA_C; 1.
 DR Pfam; PF03453; MoeA_N; 1.
 DR ProDom; PD002460; MOCF_biosynth; 1.
 DR TIGRFAMs; TIGR00177; molyb_syn; 1.
 KW complete proteome.
 SQ SEQUENCE 402 AA; 43327 MW; 44545EDA70F6A7BE CRC64;

Query Match 33.9%; Score 41; DB 17; Length 402;
 Best Local Similarity 39.1%; Pred. No. 40;
 Matches 9; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 12 SKXEEAVRLXXXXLXNGXSG 34
 DB 237 KELLIEGVADIVISGASGG 259

RESULT 11

Q96L69 PRELIMINARY; PRT; 589 AA.
 AC Q96L69;
 DT 01-DEC-2001 (TREMblrel. 19, Created)
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
 DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
 DE Ectodermal-neural cortex.
 GN ENCL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Peng Z., Zhang B., Peng X., Yuan J., Qiang B.;
 RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY049781; AL15438.1; -
 DR InterPro; IPRO00210; BTB_Poz.
 DR InterPro; IPRO06652; Kelch_red.
 DR InterPro; IPRO00165; SHPOT_acsite.
 DR Pfam; PF01344; BTB; 1.
 DR Pfam; PF01344; Kelch; 5.
 DR SMART; SM00225; BTB; 1.
 DR SMART; SM00612; Kelch; 6.
 DR PROSITE; PS50097; BTB; 1.
 DR PROSITE; PS00639; THIOI_PROTEASE_HIS; 1.
 SQ SEQUENCE 589 AA; 66113 MW; E5CE146DB8CA16E CRC64;

Query Match 33.9%; Score 41; DB 4; Length 589;
 Best Local Similarity 45.0%; Pred. No. 60;
 Matches 9; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 11 SKXEEAVRLXXXXLXNGX 30
 DB 262 SKEIVEAIRCKIKLQNDG 281

RESULT 12

Q8CTV2 PRELIMINARY; PRT; 589 AA.
 AC Q8CTV2;
 DT 01-MAR-2003 (TREMblrel. 23, Created)
 DT 01-MAR-2003 (TREMblrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
 DE Ectodermal-neural cortex 1.
 GN Mus musculus (Mouse).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=C57BL/6J;
 RA MEDLINE=22354683; PubMed=12466851;
 RA The PANTOM Consortium;
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RA "Analysis of the mouse transcriptome based on functional annotation of

RT 60,770 full-length cDNAs."
 RL Nature 420:563-573 (2002).
 DR EMBL; AK049187; BAC31597.1; -
 SQ SEQUENCE 589 AA; 66112 MW; 21EA2CA07EE6B86 CRC64;

Query Match 33.9%; Score 41; DB 11; Length 589;
 Best Local Similarity 45.0%; Pred. No. 60;
 Matches 9; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 11 SKXEEAVRLXXXXLXNGX 30
 DB 262 SKEIVEAIRCKIKLQNDG 281

RESULT 13

Q8BRG4 PRELIMINARY; PRT; 589 AA.
 AC Q8BRG4;
 DT 01-MAR-2003 (TREMblrel. 23, Created)
 DT 01-MAR-2003 (TREMblrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
 DE Ectodermal-neural cortex 1.
 GN Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=C57BL/6J;
 RA MEDLINE=22354683; PubMed=12466851;
 RA The PANTOM Consortium;
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs."
 RL Nature 420:563-573 (2002).
 DR EMBL; AK04906; BAC32136.1; -
 SQ SEQUENCE 589 AA; 66113 MW; 53C00CA49EA86B85 CRC64;

Query Match 33.9%; Score 41; DB 11; Length 589;
 Best Local Similarity 45.0%; Pred. No. 60;
 Matches 9; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 11 SKXEEAVRLXXXXLXNGX 30
 DB 262 SKEIVEAIRCKIKLQNDG 281

RESULT 14

Q9VRN8 PRELIMINARY; PRT; 2052 AA.
 AC Q9VRN8;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-OCT-2002 (TREMblrel. 22, Last sequence update)
 DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
 DE CG5406 protein.
 GN SIF OR CG5256 OR CG5406.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkeley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA April J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktoglu L., Beasley E.M.,

QY 12 KXEEAVRLXXXXLKXGXS SGA 35
 DB 1778 RQIRESVNMSIPKXFGSSGS 1801

RESULT 16

Q9VRN7 PRELIMINARY; PRT; 2072 AA.

AC Q9VRN7
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE CG5406 protein.
 GN ST OR CG5255 OR CG5406.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 CX NCBI_TaxID=7227;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=Berkley;
 RX MBDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman W.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer V., Champs M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Aitell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Bailew R.M., Baau P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Boutler J., Brokstein P., Brotler P.,
 RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Casley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pedro B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Huck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalusz F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter A.H., Wang X.,
 RA Wang Z.-Y., Wesserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang Q., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 RN [2]

RP SEQUENCE FROM N.A.
 RC Celinker S.E., Adams M.D., Krommiller B., Wan K.H., Holt R.A.,
 RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
 RA Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
 RA Carlson J.W., Center A., Champs M., Davenport L.B., Dietz S.M.,
 RA Dodson K., Dorsett V., Doup L.E., Doyle C., Drenek D., Farfan D.,
 RA Ferreira S., Frise E., Galle R.F., Garg N.S., George R.A.,
 RA Gonzalez M., Houch J., Hoskins R.A., Hostin D., Howland T.J.,
 RA Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
 RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nuno J.,
 RA Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,

RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
 RA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
 RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
 RT "Sequencing of Drosophila melanogaster genome.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]

RP SEQUENCE FROM N.A.
 RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
 RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
 RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celinker S.E.,
 RA Clump M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
 RA Krommiller B., Marshall B., Millburn G., Richter J., Russo S.,
 RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
 RT "Annotation of Drosophila melanogaster genome.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]

RP SEQUENCE FROM N.A.
 RA Adams M.D., Celinker S.E., Gibbs R.A., Rubin G.M., Venter J.C.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]

RP SEQUENCE FROM N.A.
 RC Flybase;
 RA Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RX 1 - SIMILARITY: CONTAINS 2 PH DOMAINS.
 CC EMBL, AE003565; AAF50755.3; -
 DR HSSP, P08567; IPLS.
 DR Flybase; FBgn0019652; b1f.
 DR InterPro: IPR001331; GDS_CCC24.
 DR InterPro: IPR001478; PDZ.
 DR InterPro: IPR001449; PH.
 DR InterPro: IPR003116; RBD.
 DR InterPro: IPR000219; RHOGEF.
 DR InterPro: IPR001960; WH1.
 DR Pfam; PF00169; PH; 1.
 DR Pfam; PF02196; RBD; 1.
 DR Pfam; PF00621; RHOGEF; 1.
 DR SMART; SM00228; PDZ; 1.
 DR SMART; SM00223; PH; 2.
 DR SMART; SM00455; RBD; 1.
 DR SMART; SM00325; RHOGEF; 1.
 DR SMART; SM00461; WH1; 1.
 DR PROSITE; PS00741; DH 1; 1.
 DR PROSITE; PS0010; DH 2; 1.
 DR PROSITE; PS50105; PDZ; 1.
 DR PROSITE; PS50003; PH_DOMAIN; 1.
 SQ SEQUENCE 2072 AA; 231130 MW; 3CAFE543F72DD331 CRC64;

Query Match 33.9%; Score 41; DB 5; Length 2072;
 Best Local Similarity 41.7%; Pred. No. 2.4e+02;
 Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 12 KXEEAVRLXXXXLKXGXS SGA 35
 DB 1789 RQIRESVNMSIPKXFGSSGS 1812

RESULT 17

Q9P905 PRELIMINARY; PRT; 2918 AA.

AC Q9P905
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE Filamentous haemagglutinin.
 GN FHAB OR KCCL1794.
 OS Xanthomonas campestris (pv. campestris).
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
 CC Xanthomonadaceae; Xanthomonas.
 CX NCBI_TaxID=340;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 33913 / NCPPB 528;

Query Match 33.9%; Score 41; DB 16; Length 2918;
Best Local Similarity 45.0%; Pred. No. 3,4e+02;
Matches 9; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

RA MEDLINE=22022145; PubMed=12024217;
RA da Silva A.C.R., Ferro U.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Camarotte G., Canavaro F., Cardoso J., Chambergo F., Clapina L.P.,
RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Secubal J.C., Kitajima J.P.,
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities."
RL Nature 417:459-463(2002).
DR EMBL/AB012281; AAM41083.1; -
KM Complete proteome.

SC SEQUENCE 2918 AA; 285818 MW; 4CEFA904298CE919 CRC64;

Db 16 EEAVALXXXXLKNXGXSSGA 35
2453 EQSVRLNVQSLNAGGQIGA 2472

RESULT 18
Q8PLI3 PRELIMINARY; PRT; 4753 AA.
AC Q8PLI3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Filamentous haemagglutinin.
GN PHAB OR XAC1815.
OS Xanthomonas axonopodis (pv. citri).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
CX NCBI_TaxID=92829;
[1]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=306 / ATCC 13902 / XV 101,
RX MEDLINE=22022145; PubMed=12024217;
RA da Silva A.C.R., Ferro U.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Camarotte G., Canavaro F., Cardoso J., Chambergo F., Clapina L.P.,
RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Secubal J.C., Kitajima J.P.,
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities."
RL Nature 417:459-463(2002).
DR EMBL/AB011814; AAM3677.1; -
DR InterPro: IPR000688; HYPA.
KM Pfam; PF01155; HyPa, 1.
SC Complete proteome.
SEQUENCE 4753 AA; 471484 MW; ABC4B22EB09DBF9 CRC64;

Query Match 33.9%; Score 41; DB 16; Length 4753;
Best Local Similarity 35.5%; Pred. No. 5.8e+02;
Matches 11; Conservative 2; Mismatches 18; Indels 0; Gaps 0;

QY 5 TXXXXXKQXEEAVALXXXXLKNXGXSSGA 35
Db 2452 TLDSGSKTKAESVRLNVQSLNAGGQIGA 2482

RESULT 19
P96631 PRELIMINARY; PRT; 127 AA.
AC P96631;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Probable repressor protein.
GN YDCN.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
CX NCBI_TaxID=1423;
[1]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98000887; PubMed=9341680;
RA Beloin C., Ayora S., Exley R., Hirschbein L., Ogasaawa N.,
RA Kasahara Y., Alonso J.C., Le Hegarat F.,
RT "Characterization of an lrp-like (lrpC) gene from Bacillus subtilis."
RL Mol. Genet. 256:63-71(1997).
[2]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasaawa N., Moser I., Albertini A.M., Alloni G.,
RA Azevedo V., Berteiro M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borries R., Boursier L., Brans A., Braun M., Brigelli S.C., Bron S.,
RA Brouillet S., Brusch C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Conerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
RA Eutlian K.D., Ewington J., Fader C., Ferrari E., Foulger D.,
RA Fritz C., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Goldlighty E.J., Grandi G.,
RA Giuseppe G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Medina N., Mellado R.F., Mizuno M., Moesti D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Priesgen E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadate Y.,
RA Sato T., Sannan B., Schleich S., Schroeder R., Scoffone F.,
RA Sekiguchi Y., Sekowska A., Serró S.J., Serró P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi B., Takagi T., Takahashi H., Takenaka K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Teyssie P., Tognoni A.,
RA Tosechi V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Mamout R., Medler H., Medler H., Weitzenecker T.,
RA Winiers P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumslein B., Yoshikawa H., Danchin A.,
RT "The complete genome sequence of the gram-positive bacterium Bacillus
RT subtilis."
RL Nature 390:249-256(1997).
[3]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RA Kunst F., Ogasaawa N., Yoshikawa H., Danchin A.,
RT Submitted (NOV-1997) to the EMBL/Genbank/DBJ databases.
DR EMBL/AB001488; BAA19320.1; -
DR EMBL/299106; CAB12289.1; -
DR InterPro: IPR001387; HTH_3.
KM Pfam; PF01381; HTH_3; 1.

DR SMART; SM00530; HTH_XRE; 1.
 KM Complete proteome.
 SQ SEQUENCE 127 AA; 14649 MW; 3CC91DSB1D51626C CRC64;
 Query Match 33.1%; Score 40; DB 16; Length 127;
 Best Local Similarity 47.1%; Pred. No. 18;
 Matches 8; Conservative 2; Mismatches 7; Indels 0; Gaps 0;
 QY 13 QXEEAVRLXXXXLKGK 29
 : : : : :
 100 EFDEETAPLVKXALQNG 116

RESULT 20
 ID Q9U184 PRELIMINARY; PRT; 374 AA.
 AC Q9U184;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE Hypothetical 41.7 kDa protein.
 GN L3238.06;
 OS Leishmania major.
 OC Eukaryota; Euzoenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
 OX NCBI_TaxID=5664;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Friedlin;
 RA Wedler H., Hilbert H., Duesterhoeft A., Ivens A.C., Murphy L.,
 RA Quail M., Rajandream M.A., Barrell B.G.;
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Friedlin;
 RA MEDLINE=98146435; PubMed=9477341;
 RX Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
 RA Smith D.F.;
 RT "A physical map of the Leishmania major Friedlin genome.";
 RL Genome Res. 8:135-145(1998).
 DR EMBL; AL133468; CAB6133.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 374 AA; 41675 MW; AA38847D8E433937 CRC64;

Query Match 33.1%; Score 40; DB 5; Length 374;
 Best Local Similarity 39.1%; Pred. No. 57;
 Matches 9; Conservative 4; Mismatches 10; Indels 0; Gaps 0;
 QY 12 KOXEEAVRLXXXXLKGXSSG 34
 : : : : :
 14 KOKKEAKKASGPIRGAGSSG 36

RESULT 21
 ID Q9LHL3 PRELIMINARY; PRT; 455 AA.
 AC Q9LHL3;
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE RNA-binding protein-like.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Columbia;
 RA Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Columbia;

RX MEDLINE=20363099; PubMed=10907853;
 RA Nakamura Y.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 3. II.
 RT Sequence features of the regions of 4,251,695 bp covered by ninety PL,
 RT TAC and BAC clones.";
 RL DNA Res. 7:217-221(2000).
 DR EMBL; AP002041; BAB02607.1; -.
 DR InterPro; IPR002344; Lupus_La.
 DR InterPro; IPR006630; Lupus_La.dom.
 DR InterPro; IPR00504; RNA_rec_mot.
 DR Pfam; PF00766; rrm; 1.
 DR PRINTS; PR00302; LUPUSLA.
 DR SMART; SM00715; LA; 1.
 DR SMART; SM00360; RRM; 1.
 DR PROSITE; PS0102; RRM; 1.
 SQ SEQUENCE 455 AA; 48958 MW; E88117B2C33BEA9 CRC64;

Query Match 33.1%; Score 40; DB 10; Length 455;
 Best Local Similarity 41.7%; Pred. No. 70;
 Matches 10; Conservative 3; Mismatches 11; Indels 0; Gaps 0;
 QY 12 KOXEEAVRLXXXXLKGXSSGA 35
 : : : : :
 5 QREVEGVTTBKRLDGGGSSGA 28

RESULT 22
 ID Q9GNX7 PRELIMINARY; PRT; 567 AA.
 AC Q9GNX7;
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
 DE Hypothetical 60.6 kDa protein.
 GN P1408.09;
 OS Leishmania major.
 OC Eukaryota; Euzoenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
 OX NCBI_TaxID=5664;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Friedlin;
 RA Bothe G., Pohl T., Ivens A.C., Quail M., Rajandream M.A.,
 RA Barrell B.G.;
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Friedlin;
 RX MEDLINE=98146435; PubMed=9477341;
 RA Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
 RA Smith D.F.;
 RT "A physical map of the Leishmania major Friedlin genome.";
 RL Genome Res. 8:135-145(1998).
 DR EMBL; AL358652; CAC18989.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 567 AA; 60584 MW; D311065ASB7184B9 CRC64;

Query Match 33.1%; Score 40; DB 5; Length 567;
 Best Local Similarity 40.0%; Pred. No. 89;
 Matches 8; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
 QY 15 EEEAVRLXXXXLKGXSSG 34
 : : : : :
 268 EEOKLRIVRTNLASGSSG 287

RESULT 23
 ID Q9SD72 PRELIMINARY; PRT; 609 AA.
 AC Q9SD72;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE Beta-D-glucan exohydrolase-like protein.

GN F13112.60.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Choleau N., Robert C., Brottier P., Wincker P., Catolico L.,
 RA Artiguenave F., Saurin W., Weissbach J., Mewes H.W., Lemcke K.,
 RA Mayer K.F.X., Quetier F., Salanoubat M.;
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL133292; CAB61947.1;
 DR InterPro; IPR002772; Glyco_hydro_3C.
 DR InterPro; IPR001764; Glyco_hydro_3N.
 DR Pfam; PF00933; Glyco_hydro_3; 1.
 DR Pfam; PF01915; Glyco_hydro_3; 1.
 DR PROSITE; PS00775; GLYCOSYL_HYDROL_F3; 1.
 DR HydroLase.
 SQ SEQUENCE 609 AA; 66265 MW; 35D3FAEEB83EFADA CRC64;
 Query Match 33.1%; Score 40; DB 10; Length 609;
 Best Local Similarity 38.5%; Pred. No. 96;
 Matches 10; Conservative 2; Mismatches 14; Indels 0; Gaps 0;
 OY 4 GTXXXXXSKQEEAVRLXXXXLXNG 29
 DB 376 GTVCKEHEVAREAVRKKSLVLLKNG 401
 RESULT 24
 O9SN69
 ID O9SN69 PRELIMINARY; PRT; 772 AA.
 AC O9SN69;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
 DE Hypothetical 86.7 kDa protein.
 GN F24J7.162 OR ATAG19610.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bevan M., Vitale D., Liguori R., Argirou A., De Simone V.,
 RA Bancroft I., Mewes H.W., Mayer K.F.X., Lemcke K., Schueller C.;
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Vitale D., Liguori R., Argirou A., De Simone V., Mewes H.W.,
 RA Lemcke K., Mayer K.F.X.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL021768; CAB40378.1;
 DR EMBL; AL161551; CAB78963.1;
 DR InterPro; IPR005054; RNA_rec_mot.
 DR Pfam; PF00076; ttm; 3.
 DR SMART; SM00360; RRM; 3.
 DR PROSITE; PS50102; RRM; 3.
 DR Hypothetical protein.

SQ SEQUENCE 772 AA; 86660 MW; E8AF1B53BF850FD CRC64;
 Query Match 33.1%; Score 40; DB 10; Length 772;
 Best Local Similarity 37.5%; Pred. No. 1.2e+02;
 Matches 9; Conservative 3; Mismatches 12; Indels 0; Gaps 0;
 OY 11 SKQEEAVRLXXXXLXNGXSSG 34
 DB 60 SHKKEEAKKSSSEGLKDNKAKG 83
 RESULT 25
 O8T919
 ID O8T919 PRELIMINARY; PRT; 773 AA.
 AC O8T919;
 DT 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
 DE A705602P.
 GN CG14982.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champagne M., Chavez C., Dorsett V., Dresnak D., Farran D., Frise E.,
 RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
 RA Miranda A., Mungall C.J., Nuno J., Pacble J., Parasas V., Park S.,
 RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
 RA Celinker S.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY075165; AA168036.1;
 DR FlyBase; FBgn035477; CG14982.
 SQ SEQUENCE 773 AA; 84788 MW; 080468ED1D601FCDF CRC64;
 Query Match 33.1%; Score 40; DB 5; Length 773;
 Best Local Similarity 43.5%; Pred. No. 1.2e+02;
 Matches 10; Conservative 4; Mismatches 7; Indels 2; Gaps 1;
 OY 15 EEEAV-RLXXXXLXNGXSSGA 35
 DB 129 KSEAVFERLQASVYRNGGANNGA 151
 RESULT 26
 O9VZK7
 ID O9VZK7 PRELIMINARY; PRT; 773 AA.
 AC O9VZK7;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE CG14982 protein.
 GN CG14982.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkeley;
 RX MEDLINE=20196006; PubMed=10731133;
 RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Bokova D., Botchan W.R., Bouck J., Brockstein P., Brothier P.,
 RA Butts K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodex A., Gong F., Gotreill J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.P., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegawa C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod W.P., Merverson D.,
 RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Mosnig A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.W., Weissendach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).

RP SEQUENCE FROM N.A.
 RA Evans S.E., Adams M.D., Krommiller B., Wan K.H., Holt R.A.,
 RA Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
 RA Carlson J.M., Center A., Champagne M., Davenport L.B., Dietz S.M.,
 RA Dodson K., Dorett V., Doup L.E., Doyle C., Drenek D., Farfan D.,
 RA Ferrera S., Frise E., Galle R.F., Garg N.S., George R.A.,
 RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
 RA Idegawa C., Jalali M., Kruse D., Li P., Mattei B., Mosnig A.,
 RA McIntosh T.C., Moy M., Murphy B., Nelson K.A., Nunoo J.,
 RA Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,
 RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
 RA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
 RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
 RT "Sequencing of *Drosophila melanogaster* genome.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

RP SEQUENCE FROM N.A.
 RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
 RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
 RA Tupy J.L., Bergman C., Berman C., Carlson J.M., Celniker S.E.,
 RA Clamp M., Drysdale R., Emmett D., Frise E., de Grey A., Harris N.,
 RA Krommiller B., Marshall B., Milburn G., Richter J., Russo S.,
 RA Searte S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
 RT "Annotation of *Drosophila melanogaster* genome.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RP SEQUENCE FROM N.A.
 RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter J.C.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RP SEQUENCE FROM N.A.
 RA EMBL; A5003479; AAF47814.2; -
 DR Flybase: FBgn035477; CG14982.
 SO SEQUENCE 773 AA; 84832 MW; E1D9789DE2AD912C CRC64;

Query Match 33.1%; Score 40; DB 5; Length 773;
 Best Local Similarity 43.5%; Pred. No. 1.2e+02;
 Matches 10; Conservative 4; Mismatches 7; Indels 2; Gaps 1;

OY 15 EEEAV--RLXXXXLXNGXSSGA 35
 Db 129 KSEAVFERLQAGSYRNGGNGGA 151

RESULT 27
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 AC OYKX3;
 DT 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
 DT 01-OCT-2002 (TREMblrel. 22, Last annotation update)
 DE Adhesin like-protein P146.
 GN P146.
 OS Mycoplasma hyopneumoniae.
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
 OX NCBI_TaxID=2099;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BO14;
 RA Verdin E., Saillard C.;
 RT "Adjacent sequence of Mycoplasma hyopneumoniae ABC transporter P11 and P12.";
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF279908; AAF91425.1; -
 SO SEQUENCE 1296 AA; 146344 MW; 024ECB30C12D9670 CRC64;

Query Match 33.1%; Score 40; DB 2; Length 1296;
 Best Local Similarity 39.1%; Pred. No. 2.2e+02;
 Matches 9; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

OY 12 KOXEEAVRLXXXXLXNGXSSG 34
 Db 960 KKYERSSKYVGTENNNGSSSG 982

RESULT 28
 OYKX4 PRELIMINARY; PRT: 2382 AA.
 ID OYKX4;
 DT 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
 DT 01-OCT-2002 (TREMblrel. 22, Last annotation update)
 DE L712.16.
 GN L712.16.
 OS Leishmania major.
 OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
 OX NCBI_TaxID=5664;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Friedlin;
 RA Myler P.J.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Friedlin;
 RA Worthey E.A., Sisk E., Hixson G., Kiser P., Rickel E., Hassebrock M.,
 RA Cawthra J., Sunkin S., Stuart K.D., Myler P.J.;
 RT "Direct Submission.";
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC005930; AAF9730.1; -
 DR EMBL; AC125735; AAF69050.1; -
 SO SEQUENCE 2382 AA; 250422 MW; 838E575E5927E737 CRC64;

Query Match 33.1%; Score 40; DB 5; Length 2382;
 Best Local Similarity 38.1%; Pred. No. 4.2e+02;
 Matches 8; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

OY 13 OXEEAVRLXXXXLXNGXSS 33
 Db 1352 QRSHEKVLISAAGYKNGSSAA 1372

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RESULT 29
ID P70746 PRELIMINARY; PRT; 145 AA.
AC P70746;
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Cysteine biosynthesis protein CysC (Fragment).
GN CysC.
OS Aeromonas hydrophila.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=644;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JMP636;
RA Ingham A.B., Pemberton J.M.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U76718; AAB18818.1; -.
DR HSSP; P38038; 1DDG.
DR InterPro; IPR001097; FAD binding.
DR Pfam; PF00667; FAD_binding_1; 1.
DR PRINTS; PF00258; Flavodoxin; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 145 AA; 145 MW; 13170F0D9FAE37B CRC64;

Query Match 32.2%; Score 39; DB 2; Length 145;
Best Local Similarity 36.0%; Pred. No. 31;
Matches 9; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

QY 11 SKQXEEAVRLXXXXLKNQXSSGA 35
DB 36 AKWGEQAVKAIATLTLSAGAAAPAA 60

RESULT 30
ID O58594 PRELIMINARY; PRT; 208 AA.
AC O58594;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE 208AA long hypothetical transcription initiation factor IIB.
GN PH0864.
OS Pyrococcus horikoshii.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=51953;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OT3;
RX MEDLINE=98344137; PubMed=9679194;
RA Kawarabayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
RA Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kishida N., Oguchi A.,
RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
RA Masuchi Y., Shizuya H., Kikuchi H.;
RT "Complete sequence and gene organization of the genome of a hyper-
RT thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";
RL DNA Res. 5:55-76(1998).
DR EMBL; AP000003; BAA2958.1; -.
DR HSSP; P29095; 1A1S.
DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR000812; TFIIB euk.
DR Pfam; PF00382; Transcription_Fac2; 2.
DR PRINTS; PRO0685; TIFACTOR1B.
DR SMART; SM00385; CYCLIN; 2.
DR PROSITE; PS00782; TFIIB; 1.
KW Initiation factor; Complete proteome.

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SQ SEQUENCE 208 AA; 23878 MW; CBE1A3D30CC76762 CRC64;

Query Match 32.2%; Score 39; DB 17; Length 208;
Best Local Similarity 44.4%; Pred. No. 46;
Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 12 KOXEEAVRLXXXXLKNQ 29
DB 38 KHYREAVRIYRKLKSG 55

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Search completed: December 23, 2003, 10:03:49
Job time : 31.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 23, 2003, 09:59:55 : Search time 36.5 Seconds
(without alignments)
173.947 Million cell updates/sec

Title: US-09-889-331a-48
Perfect score: 112
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Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the total score being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	79	70.5	38	21	AA52839
2	71.5	63.8	37	20	AA17618
3	71.5	63.8	37	22	AAE08527
4	71.5	63.8	37	22	AAE04363
5	71.5	63.8	39	21	AA11313
6	71.5	63.8	39	22	AAE08383
7	70.5	62.9	36	20	AA17606
8	70.5	62.9	36	21	AA11263
9	70.5	62.9	36	21	AA53029

10	70.5	62.9	36	21	AA194184	Amino acid sequenc
11	70.5	62.9	36	22	AAE08515	Extendin agonist pe
12	70.5	62.9	36	22	AAE04351	Extendin agonist, S
13	70.5	62.9	37	20	AA124869	Extendin agonist pe
14	70.5	62.9	37	20	AA124853	Extendin agonist pe
15	70.5	62.9	37	20	AA124854	Extendin agonist pe
16	70.5	62.9	37	21	AA11275	Extendin agonist pe
17	70.5	62.9	37	21	AAE08304	Extendin agonist c
18	70.5	62.9	37	21	AA194196	Amino acid sequenc
19	70.5	62.9	37	22	AAE08427	Extendin agonist pe
20	70.5	62.9	37	22	AAE08428	Extendin agonist pe
21	70.5	62.9	37	22	AAE08443	Extendin agonist pe
22	70.5	62.9	37	22	AAE04263	Extendin agonist, S
23	70.5	62.9	37	22	AAE04264	Extendin agonist, S
24	70.5	62.9	39	22	AAE04279	Extendin agonist, S
25	70.5	62.9	39	21	AA11311	Extendin agonist pe
26	70.5	62.9	39	21	AA194039	Amino acid sequenc
27	70.5	62.9	39	21	AA194040	Amino acid sequenc
28	70.5	62.9	39	21	AA194043	Extendin agonist pe
29	70.5	62.9	39	22	AAE08379	Extendin agonist pe
30	70.5	62.9	39	22	AAE08380	Extendin agonist pe
31	70.5	62.9	39	22	AAE08381	Extendin agonist pe
32	70.5	62.9	39	22	AAE04219	Extendin agonist, S
33	69.5	62.1	35	20	AA11535	Extendin agonist pe
34	69.5	62.1	35	20	AA124839	Extendin agonist pe
35	69.5	62.1	35	20	AA124839	Extendin agonist pe
36	69.5	62.1	35	21	AA11161	Extendin agonist pe
37	69.5	62.1	35	21	AA11161	Extendin agonist pe
38	69.5	62.1	35	21	AAE08290	Extendin agonist c
39	69.5	62.1	35	21	AAE08301	Extendin agonist c
40	69.5	62.1	35	21	AA194074	Amino acid sequenc
41	69.5	62.1	35	21	AA194186	Amino acid sequenc
42	69.5	62.1	35	22	AAE08413	Extendin agonist pe
43	69.5	62.1	35	22	AAE08417	Extendin agonist pe
44	69.5	62.1	35	22	AAE08429	Extendin agonist, S
45	69.5	62.1	35	22	AAE04353	Extendin agonist, S
46	69.5	62.1	36	20	AA11533	Extendin agonist pe
47	69.5	62.1	36	20	AA124856	Extendin agonist pe
48	69.5	62.1	36	20	AA124837	Extendin agonist pe
49	69.5	62.1	36	20	AA124837	Extendin agonist pe
50	69.5	62.1	36	20	AA17605	Extendin agonist pe

ALIGNMENTS

RESULT 1	
AA52839	standard; Peptide: 38 AA.
AA52839:	
XX	
AC	
XX	
DT	
XX	
DE	Extendin agonist peptide #9.
XX	
KW	Extendin; agonist; diabetes; obesity; eating disorder;
KV	dyslipidemia; insulin-resistance syndrome; food intake.
XX	
OS	Heloderma sp.
XX	
PN	W020006629-A1.
XX	
PD	09-NOV-2000.
XX	
PF	28-APR-2000; 2000WO-US11814.
XX	
FR	30-APR-1999; 99US-0132018.
XX	
PA	(AMYL-) AMYLIN PHARM INC.
XX	
PI	Young A, Prickett K;
XX	

DR WPI: 2000-672834/65.
XX
XX Modified extendin or an extendin agonist linked to one or more
PT polyethylene glycol (PEG) polymers, modulate plasma glucose levels,
XX useful for treating disorders such as diabetes and obesity -
XX
PS Disclosure; Page 52-53; 119pp; English.

XX The present invention relates to extendins and their agonists which have
CC been modified with molecular weight increasing agents such as
CC polyethylene glycol (PEG). These can be used in the treatment of
CC diabetes, obesity, impaired glucose tolerance, postprandial dumping
CC syndrome, postprandial hyperglycaemia, eating disorders, insulin
CC resistance syndrome, dyslipidaemia and to suppress glucagon secretion.
XX
SQ Sequence 38 AA;

Query Match 70.5%; Score 79; DB 21; Length 38;
Best Local Similarity 100.0%; Pred. No. 8e-08;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 GTXXXXXXSKQEEAVRLXXXXLXGXS SGA 34
DB 4 GTXXXXXXSKQEEAVRLXXXXLXGXS SGA 34

RESULT 2

AAV17618
ID AAV17618 standard; peptide: 37 AA.

XX AAV17618;

XX 09-AUG-1999 (first entry)

XX Extendin agonist peptide #84.

XX Extendin; agonist; Heloderma sp.; Gila monster; venom; lizard;

XX diabetes mellitus type I; diabetes mellitus type II; hyperglycaemia;

XX hypoglycaemia; plasma glucose; gastric emptying; stomach emptying.

XX Synthetic.

XX Heloderma sp.

XX WO9925728-A1.

XX 27-MAY-1999.

XX 13-NOV-1998; 98WO-US24273.

XX 14-NOV-1997; 97US-0066029.

XX (AMYL-) AMYLIN PHARM INC.

XX Beeley NRA, Prickett KS;

XX WPI: 1999-347456/29.

XX Peptide agonists of extendin - delay stomach emptying, for treating

XX diabetes and hypo- or hyper-glycaemia

XX Claim 28; Fig 4; 144pp; English.

XX AA17535 to AAV17624 represent extendin peptide agonists. Extendins are
CC peptides that are found in the venom of the Gila monster, a lizard
CC endogenous to Arizona and Northern Mexico. The peptide agonists are
CC used to treat diabetes mellitus (types I or II), hyperglycaemia or
CC hypoglycaemia. They can also be used for in vitro and in vivo studies
CC on extendins and their agonists. They regulate gastric motility and slow
CC gastric emptying (resulting in lower post-prandial glucose levels).

XX Sequence 37 AA;

Query Match

63.8%; Score 71.5; DB 20; Length 37;

Best Local Similarity 59.4%; Pred. No. 2.1e-06;
Matches 19; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

OY 4 GTXXXXXXSKQEEAVRLXXXXLXGXS SGA 34
DB 4 GTFTSLSKQEEAVRLFTLWLNKXGXS SGA 35

RESULT 3

AAE08527
ID AAE08527 standard; peptide: 37 AA.

XX AAE08527;

XX 01-NOV-2001 (first entry)

XX Extendin agonist peptide #172.

XX Extendin agonist; antidiabetic; cardiac; triglyceride; inotropic;

XX diuretic; coronary heart disease; dyslipidaemia.

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 31 /note= "N-methyl alanine"

FT Modified-site 36 /note= "N-methyl alanine"

FT Modified-site 37 /note= "N-methyl alanine; C-terminal amide"

XX WO200151078-A1.

XX 19-JUL-2001.

XX 09-JAN-2001; 2001WO-US00719.

XX 10-JAN-2000; 2000US-0175365.

XX (AMYL-) AMYLIN PHARM INC.

XX Kolterman OG, Young AA;

XX WPI: 2001-514422/56.

XX Use of extendin and extendin agonist compounds for modulating

XX triglyceride levels, and treating heart disease and dyslipidemia -

XX Example 178; Page 143; 161pp; English.

XX The patent discloses a method for modulating plasma or postprandial
CC triglyceride and other lipid levels by administering extendin or an
CC extendin agonist. Extendins have inotropic and diuretic effects. They
CC suppress the secretion of glucagon. Extendin and its agonists have
CC a significant effect on the reduction of blood serum triglyceride
CC concentrations. They are used to treat coronary heart disease and
CC dyslipidaemia, and for modifying postprandial triglyceride levels.
XX The present peptide sequence is an agonist of extendin.

XX Sequence 37 AA;

Query Match 63.8%; Score 71.5; DB 22; Length 37;
Best Local Similarity 59.4%; Pred. No. 2.1e-06;
Matches 19; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

OY 4 GTXXXXXXSKQEEAVRLXXXXLXGXS SGA 34
DB 4 GTFTSLSKQEEAVRLFTLWLNKXGXS SGA 35

RESULT 4

AAE64363
ID AAE64363 standard; peptide: 37 AA.

XX AAB64363;
AC
XX
XX 27-MAR-2001 (first entry)
DT
XX
XX
DE Exendin agonist, SEQ ID NO:183.
XX
XX Exendin agonist; gestational diabetes mellitus; GDM; insulin resistance;
XX pregnancy complication; neonatal abnormality; blood glucose modulator;
XX insulinotropic; anorectic; exendin-4.
XX
XX Heloderma suspectum.
OS
XX Synthetic.
XX
XX WO200073331-A2.
XX
XX 07-DEC-2000.
PD
XX
XX 23-MAY-2000; 2000WO-US14231.
PF
XX
XX 01-JUN-1999; 99US-0323867.
PR
XX
XX (AMYL-) AMYLIN PHARM INC.
PA
XX
XX Hiles R, Prickett KS;
PI
XX
XX WPI; 2001-137634/14.
DR
XX
XX Use of exendins or exendin agonists for lowering or reducing blood
PT glucose levels and treating gestational diabetes mellitus in a subject,
PT especially in a human -
XX
XX Example 178; Page 119; 133pp; English.
PS
XX
XX The invention relates to the use of an exendin (AAB64181-B64182) or
CC an exendin agonist (AAB64185-B64368) for treating gestational diabetes
CC mellitus (GDM) in a patient. GDM arises during pregnancy, and is due
CC to a combination of increased insulin resistance and a diminished
CC ability to increase insulin secretion. In contrast, in a normal
CC pregnancy, both insulin resistance and insulin secretion increase. GDM
CC pregnancies are associated with complications in both the mother and the
CC foetus. Women with GDM have increased rates of Caesarian delivery,
CC hypertensive disorders such as pre-eclampsia, and urinary tract
CC infections. GDM results in an elevated rate of foetal abnormalities such
CC as neural tube defects, and is associated with an increased risk of
CC neonatal morbidities such as hypoglycaemia, hypocalcaemia,
CC hypomagnesaemia, polycythaemia, hyperbilirubinaemia, and subsequent
CC childhood and adolescent obesity. Exendins are peptides from the salivary
CC secretions of the Gila monster (exendin-4) and the Mexican beaded lizard
CC (exendin-3) which exhibit homology with several members of the
CC glucagon-like peptide family, particularly GLP-1, and have similar
CC insulinotropic effects. Unlike the compounds used to treat type 2
CC diabetes, which are contraindicated for GDM, exendins and exendin
CC agonists do not cross the placenta and thus do not cause severe prolonged
CC hypoglycaemia in the newborn. They have a potent and prolonged effect on
CC blood glucose, and, unlike conventional insulin therapy, should not cause
CC weight gain, as they inhibit gastric emptying and reduce appetite. The
CC present sequence represents a exendin agonist of the invention which is
CC based upon the sequence of exendin-4.
XX
SQ Sequence 37 AA;
Query Match 63.8%; Score 71.5; DB 22; Length 37;
Best Local Similarity 59.4%; Pred. No. 2.1e-06;
Matches 19; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

ID AAB11313 standard; Peptide; 39 AA.
XX
XX AAB11313;
AC
XX
XX 20-FEB-2001 (first entry)
DT
XX
XX
DE Exendin agonist peptide SEQ ID NO 39.
XX
XX Exendin agonist; treatment; antidiabetic; insulin sensitivity; diabetes;
XX plasma glucose; gastric emptying; food intake.
XX
XX Synthetic.
OS
XX
XX WO2000041546-A2.
XX
XX 20-JUL-2000.
PD
XX
XX 10-JAN-2000; 2000US-0116380.
PF
XX
XX 14-JAN-1999; 99US-0116380.
PR
XX
XX (AMYL-) AMYLIN PHARM INC.
PA
XX
XX Young A, L'Italien JJ, Kolterman O;
PI
XX
XX WPI; 2000-514584/46.
DR
XX
XX New formulations comprising an exendin or exendin agonist peptide used
PT for increasing the sensitivity of a subject to insulin to treat
PT diabetes -
XX
XX Example 44; Figure 15; 281pp; English.
PS
XX
XX This invention describes a novel formulation (I) comprising an exendin or
CC exendin agonist peptide, a buffer and an iso-osmolality modifier which
CC has a pH of 3-7. The products of the invention have antidiabetic
CC activity. The exendin or exendin agonist is used to increase the
CC sensitivity of a subject to insulin to treat diabetes and disorders
CC which would benefit from agents which lower plasma glucose levels and disorders
CC which would benefit from agents that delay and/or slow gastric emptying
CC or reducing food intake.
XX
SQ Sequence 39 AA;
Query Match 63.8%; Score 71.5; DB 21; Length 39;
Best Local Similarity 59.4%; Pred. No. 2.2e-06;
Matches 19; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

QY 4 GTXXXXXSKQEEAEVRLXXXXL-XGXSSGA 34
DB 4 GTTSDLSKQEEAEVRLFIETLKNKGASGA 35

RESULT 6
AAE08383
ID AAE08383 standard; peptide; 39 AA.
XX
XX AAE08383;
AC
XX
XX 01-NOV-2001 (first entry)
DT
XX
XX
DE Exendin agonist peptide #30.
XX
XX Exendin agonist; antilipemic; cardiact; triglyceride; inotropic;
XX diuretic; coronary heart disease; dyslipidaemia.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH Modified-site 31 /note= "N-Methyl-alanine"
FT Modified-site 36 /note= "N-Methyl-alanine"
FT

FT Modified-site 37 /note= "N-Methyl-alanine"
 FT Modified-site 38 /note= "N-Methyl-alanine"
 FT Modified-site 39 /note= "C-terminal amide"
 FT WO200151078-A1.
 PN 19-JUL-2001.
 PD 09-JAN-2001; 2001WO-US00719.
 PF 10-JAN-2000; 2000US-0175365.
 PR (AMYL-) AMYLIN PHARM INC.
 PA Kolterman OG, Young AA;
 PI WPI; 2001-514422/56.
 DR Use of exendin and exendin agonist compounds for modulating
 PT triglyceride levels, and treating heart disease and dyslipidemia
 PS Example 30; Page -; 161pp; English.
 XX The patent discloses a method for modulating plasma or postprandial
 CC triglyceride and other lipid levels by administering exendin or an
 CC exendin agonist. Exendins have inotropic and diuretic effects. They
 CC suppress the secretion of glucagon. Exendin and its agonists have
 CC a significant effect on the reduction of blood serum triglyceride
 CC concentrations. They are used to treat coronary heart disease and
 CC dyslipidaemia, and for modifying postprandial triglyceride levels.
 CC Note: The present sequence is an agonist of exendin.
 CC derived from SEQ ID NO:3 shown in page 17 of the specification.
 XX
 SQ Sequence 39 AA;
 QY Query Match 63.8%; Score 71.5; DB 22; Length 39;
 Best Local Similarity 59.4%; Pred. No. 2.2e-06;
 Matches 19; Conservative 0; Mismatches 12; Indels 1; Gaps 1;
 DB 4 GTXXXXXSKQEEAVRLXXXXL-XGXSXSGA 34
 4 GTFTSDLSKQLEEAVALFTFELKNGXSSGA 35
 RESULT 7
 AA17606
 ID AA17606 standard; peptide; 36 AA.
 AC AA17606;
 XX 09-AUG-1999 (first entry)
 DT Exendin agonist peptide #72.
 DE Exendin agonist peptide #72.
 XX Exendin; agonist; Heloderma sp.; Gila monster; venom; lizard.
 KW diabetes mellitus type I; diabetes mellitus type II; hyperglycaemia;
 KM hypoglycaemia; plasma glucose; gastric emptying; stomach emptying.
 XX Synthetic.
 OS Heloderma sp.
 PN WO9925728-A1.
 PD 27-MAY-1999.
 XX 13-NOV-1998; 98WO-US24273.
 PF 14-NOV-1997; 97US-0066029.
 PR
 XX

PA (AMYL-) AMYLIN PHARM INC.
 XX Beley NRA, Prickett KS;
 PI WPI; 1999-347456/29.
 DR Peptide agonists of exendin - delay stomach emptying, for treating
 XX diabetes and hypo- or hyper-glycaemia
 PT Claim 28; Fig 4; 14pp; English.
 PS
 XX AA17535 to AA17624 represent exendin peptide agonists. Exendins are
 CC peptides that are found in the venom of the Gila-monster, a lizard
 CC endogenous to Arizona and Northern Mexico. The peptide agonists are
 CC used to treat diabetes mellitus (types I or II), hyperglycaemia or
 CC hypoglycaemia. They can also be used for in vitro and in vivo studies
 CC on exendins and their agonists. They regulate gastric motility and slow
 CC gastric emptying (resulting in lower post-prandial glucose levels).
 XX
 SQ Sequence 36 AA;
 QY Query Match 62.9%; Score 70.5; DB 20; Length 36;
 Best Local Similarity 59.4%; Pred. No. 3.2e-06;
 Matches 19; Conservative 0; Mismatches 12; Indels 1; Gaps 1;
 DB 4 GTXXXXXSKQEEAVRLXXXXL-XGXSXSGA 34
 4 GTFTSDLSKQLEEAVALFTFELKNGXSSGA 35
 RESULT 8
 AA11263
 ID AA11263 standard; Peptide; 36 AA.
 AC AA11263;
 XX 20-FEB-2001 (first entry)
 DT exendin agonist peptide SEQ ID NO 171.
 DE Exendin; agonist; treatment; antidiabetic; insulin sensitivity; diabetes;
 XX plasma glucose; gastric emptying; food intake.
 KM Synthetic.
 OS
 XX WO200041546-A2.
 XX 20-JUL-2000.
 PD 10-JAN-2000; 2000US-0116380.
 PF 14-JAN-1999; 99US-0116380.
 PR (AMYL-) AMYLIN PHARM INC.
 PA Young A, L'italien JJ, Kolterman O;
 PI WPI; 2000-514584/46.
 DR New formulations comprising an exendin or exendin agonist peptide used
 XX for increasing the sensitivity of a subject to insulin to treat
 PT diabetes -
 XX Example 180; Page 229; 281pp; English.
 XX This invention describes a novel formulation (I) comprising an exendin or
 CC exendin agonist peptide, a buffer and an iso-osmolality modifier which
 CC has a pH of 3-7. The products of the invention have antidiabetic
 CC activity. The exendin or exendin agonist is used to increase the
 CC sensitivity of a subject to insulin to treat diabetes and disorders which
 CC would benefit from agents which lower plasma glucose levels and disorders
 CC which would benefit from agents that delay and/or slow gastric emptying
 CC or reducing food intake.

XX Sequence 36 AA;
SQ
Query Match 62.9%; Score 70.5; DB 21; Length 36;
Best Local Similarity 59.4%; Pred. No. 3.2e-06;
Matches 19; Conservative 0; Mismatches 12; Indels 1; Gaps 1;
QY 4 GTXXXXXSKQXEEAVRLXXXXL-XGXSXSGA 34
DB 4 GTFTSDASKQLEBEAVRLFIFLKNKGSPSSGA 35

RESULT 9
AAB53029
ID AAB53029 standard; Peptide; 36 AA.
AC AAB53029;
DT 28-FEB-2001 (first entry)
XX
XX Extendin agonist compound #157.
DE
DE Extendin agonist; diabetes; obesity; eating disorder;
KW dyslipidaemia; insulin-resistance syndrome; food intake.
XX
XX Heloderma sp.
OS
PN WQ200066629-A1.
XX
PD 0%-NOV-2000.
XX
PF 28-APR-2000; 2000WO-US11814.
XX
PR 30-APR-1999; 99US-0132018.
XX
XX (AMYL-) AMYLIN PHARM INC.
PA
PI Young A, Prickett K;
XX
XX WPI; 2000-672834/65.
DR
XX
XX Modified extendin or an extendin agonist linked to one or more
PT polyethylene glycol (PEG) polymers, modulate plasma glucose levels,
PT useful for treating disorders such as diabetes and obesity -
PS
XX Disclosure; Fig 4; 119pp; English.
XX
XX The present invention relates to extendins and their agonists which have
CC been modified with molecular weight increasing agents such as
CC polyethylene glycol (PEG). These can be used in the treatment of
CC diabetes, obesity, impaired glucose tolerance, postprandial dumping
CC syndrome, postprandial hyperglycaemia, eating disorders, insulin
CC resistance syndrome, dyslipidaemia and to suppress glucagon secretion.
XX
SQ Sequence 36 AA;
Query Match 62.9%; Score 70.5; DB 21; Length 36;
Best Local Similarity 59.4%; Pred. No. 3.2e-06;
Matches 19; Conservative 0; Mismatches 12; Indels 1; Gaps 1;
QY 4 GTXXXXXSKQXEEAVRLXXXXL-XGXSXSGA 34
DB 4 GTFTSDASKQLEBEAVRLFIFLKNKGSPSSGA 35

RESULT 10
AAY94184
ID AAY94184 standard; peptide; 36 AA.
AC AAY94184;
XX
XX 20-OCT-2000 (first entry)
DT
XX

DE Amino acid sequence of an extendin agonist.
XX
XX Extendin; Gila monster lizard; Mexican Beaded lizard; agonist;
KW glucagon-like peptide; plasma glucagon; necrolytic erythema;
KW glucagonoma; hyperglucagonemia; diabetes.
XX
XX Synthetic.
OS Heloderma sp.
FH
FH Key Location/Qualifiers
FT Modified-site 36
FT FT /note= "amidated residue"
XX
XX WQ200041548-A2.
XX
XX 20-JUL-2000.
PD
XX 14-JAN-2000; 2000WO-US00942.
PF
XX 14-JAN-1999; 99US-0116380.
PR 30-APR-1999; 99US-0132017.
PR 10-JAN-2000; 2000US-0175365.
XX
XX (AMYL-) AMYLIN PHARM INC.
PA
PI Young A, Gedulin B;
XX
XX WPI; 2000-490999/43.
DR
XX
XX Lowering plasma glucagon using extendin, an extendin agonist, a modified
PT extendin or a modified extendin agonist, useful for treating
PT hyperglucagonemia and diabetes -
XX
XX
PS Disclosure; Fig 4G; 96pp; English.
XX
XX The present sequence represents a modified extendin or extendin agonist.
CC Extending are found in the salivary glands of the Gila monster and
CC Mexican Beaded lizard, and have sequence similarity to glucagon-like
CC peptides. They are used in the method of the invention. The specification
CC describes a method for lowering plasma glucagon, comprising administering
CC an extendin, an extendin agonist, a modified extendin or a modified
CC agonist. These compounds lower plasma glucagon level. The method is
CC useful for lowering plasma glucagon in subjects, preferably humans,
CC suffering from necrolytic erythema or glucagonoma. The method is also
CC useful for treating hyperglucagonemia and other conditions that would
CC benefit from reduced glucagon levels and/or suppression of glucagon,
CC e.g. type 1 and type 2 diabetes.
XX
SQ Sequence 36 AA;
Query Match 62.9%; Score 70.5; DB 21; Length 36;
Best Local Similarity 59.4%; Pred. No. 3.2e-06;
Matches 19; Conservative 0; Mismatches 12; Indels 1; Gaps 1;
QY 4 GTXXXXXSKQXEEAVRLXXXXL-XGXSXSGA 34
DB 4 GTFTSDASKQLEBEAVRLFIFLKNKGSPSSGA 35

RESULT 11
AAE08515
ID AAE08515 standard; peptide; 36 AA.
AC AAE08515;
XX
XX 01-NOV-2001 (first entry)
DT
XX
XX Extendin agonist peptide #160.
DE
XX Extendin agonist; antilipemic; cardiant; triglyceride; inotropic;
KW diuretic; coronary heart disease; dyslipidaemia.
XX
OS Synthetic.

XX Key Location/Qualifiers
 FT Modified-site 36
 FT /note= "C-terminal amide"
 XX
 XX WO200151078-A1.
 XX
 XX PD 19-JUL-2001.
 XX
 XX PF 09-JAN-2001; 2001WO-US00719.
 XX
 XX PR 10-JAN-2000; 2000US-0175365.
 XX
 XX PA (AMYL-) AMYLIN PHARM INC.
 XX
 XX PI Kolterman OG, Young AA;
 XX
 XX DR WPI; 2001-514422/56.
 XX
 XX PT Use of exendin and exendin agonist compounds for modulating
 PT triglyceride levels, and treating heart disease and dyslipidemia
 PS Example 166; Page 136; 161pp; English.
 CC The patent discloses a method for modulating plasma or postprandial
 CC triglyceride and other lipid levels by administering exendin or an
 CC exendin agonist. Exendins have inotropic and diuretic effects. They
 CC suppress the secretion of glucagon. Exendin and its agonists have
 CC a significant effect on the reduction of blood serum triglyceride
 CC concentrations. They are used to treat coronary heart disease and
 CC dyslipidemia, and for modifying postprandial triglyceride levels.
 CC The present peptide sequence is an agonist of exendin.
 XX
 SQ Sequence 36 AA;
 Query Match 62.9%; Score 70.5; DB 22; Length 36;
 Best Local Similarity 59.4%; Pred. No. 3.2e-06;
 Matches 19; Conservative 0; Mismatches 12; Indels 1; Gaps 1;
 QY 4 GTXXXXXSKQEEAVRLXXXXL-XGQXSSGA 34
 DB 4 GTFTSDASKQLEEAVALFIEFLKNQGPSSGA 35

RESULT 12
 AAB64351
 ID AAB64351 standard; peptide; 36 AA.
 XX
 AC AAB64351;
 XX
 DT 27-MAR-2001 (first entry)
 XX
 DE Exendin agonist, SEQ ID NO:171.
 XX
 KM Exendin agonist; gestational diabetes mellitus; GDM; insulin resistance;
 KM pregnancy complication; neonatal abnormality; blood glucose modulator;
 KM insulinotropic; anorectic; exendin-4.
 XX
 OS Heloderma suspectum.
 OS Synthetic.
 XX
 PN WO200073331-A2.
 XX
 PD 07-DEC-2000.
 XX
 PF 23-MAY-2000; 2000WO-US14231.
 XX
 PR 01-JUN-1999; 99US-033867.
 XX
 PA (AMYL-) AMYLIN PHARM INC.
 XX
 PI Hiles R, Prickett KS;
 XX

DR WPI; 2001-137634/14.
 XX
 XX PT Use of exendins or exendin agonists for lowering or reducing blood
 PT glucose levels and treating gestational diabetes mellitus in a subject,
 PT especially in a human -
 XX
 XX PS Example 166; Page 133; 133pp; English.
 XX
 XX CC The invention relates to the use of an exendin (AAB64181-B64182) or
 CC an exendin agonist (AAB64185-B64368) for treating gestational diabetes
 CC mellitus (GDM) in a patient. GDM arises during pregnancy, and is due
 CC to a combination of increased insulin resistance and a diminished
 CC ability to increase insulin secretion. In contrast, in a normal
 CC pregnancy, both insulin resistance and insulin secretion increase. GDM
 CC pregnancies are associated with complications in both the mother and the
 CC foetus. Women with GDM have increased rates of Caesarian delivery,
 CC hypertensive disorders such as pre-eclampsia, and urinary tract
 CC infections. GDM results in an elevated rate of foetal abnormalities such
 CC as neural tube defects, and is associated with an increased risk of
 CC neonatal morbidities such as hypoglycaemia, hypocalcaemia,
 CC hypomagnesaemia, polycythaemia, hyperbilirubinaemia, and subsequent
 CC childhood and adolescent obesity. Exendins are peptides from the salivary
 CC secretions of the Gila monster (exendin-4) and the Mexican bearded lizard
 CC (exendin-3) which exhibit homology with several members of the
 CC glucagon-like peptide family, particularly GLP-1, and have similar
 CC insulinotropic effects. Unlike the compounds used to treat type 2
 CC diabetes, which are contraindicated for GDM, exendins and exendin
 CC agonists do not cross the placenta and thus do not cause severe prolonged
 CC hypoglycaemia in the newborn. They have a potent and prolonged effect on
 CC blood glucose, and, unlike conventional insulin therapy, should not cause
 CC weight gain, as they inhibit gastric emptying and reduce appetite. The
 CC present sequence represents a exendin agonist of the invention which is
 CC based upon the sequence of exendin-4.
 XX
 SQ Sequence 36 AA;
 Query Match 62.9%; Score 70.5; DB 22; Length 36;
 Best Local Similarity 59.4%; Pred. No. 3.2e-06;
 Matches 19; Conservative 0; Mismatches 12; Indels 1; Gaps 1;
 QY 4 GTXXXXXSKQEEAVRLXXXXL-XGQXSSGA 34
 DB 4 GTFTSDASKQLEEAVALFIEFLKNQGPSSGA 35

RESULT 13
 AAY24869
 ID AAY24869 standard; peptide; 37 AA.
 XX
 AC AAY24869;
 XX
 DT 24-AUG-1999 (first entry)
 XX
 DE Exendin agonist peptide #61.
 XX
 KM Exendin; agonist; Heloderma sp.; Gila monster; venom; lizard;
 KM diabetes mellitus type I; diabetes mellitus type II; hypoglycaemia;
 KM hypoglycaemia; plasma glucose; gastric emptying; stomach emptying.
 XX
 OS Synthetic.
 OS Heloderma sp.
 XX
 PN WO9925727-A2.
 XX
 PD 27-MAY-1999.
 XX
 PF 13-NOV-1998; 98WO-US24210.
 XX
 PR 14-NOV-1997; 97US-0065442.
 XX
 PA (AMYL-) AMYLIN PHARM INC.
 XX
 PI Beeley NRA, Prickett KS;
 XX

XX DR WPI; 1999-394773/33.
 XX PT New extendin agonist peptides - can regulate gastric motility and
 XX PT slow gastric emptying, used for treating, e.g. diabetes
 PS Claim 18; Fig 4; 108bp; English.
 CC AAY24809 to AAY24877 represent extendin agonist peptides which can
 CC regulate gastric motility and slow gastric emptying. The peptides can be
 CC used for treating e.g. diabetes or hyperglycaemic or hypoglycaemic
 CC conditions. The peptides are extendin agonists which have activity as
 CC agents to regulate gastric motility and to slow gastric emptying, as
 CC evidenced by the ability to reduce post-prandial glucose levels in
 CC mammals. They can be used for the treatment of Type I and II diabetes and
 CC hyperglycaemic or hypoglycaemic conditions. They can also be used for the
 CC treatment of disorders which would be benefited by agents which lower
 CC plasma glucose levels and in treatment of disorders which would be
 CC benefited with agents useful in delaying and/or slowing gastric
 CC emptying.
 SQ Sequence 37 AA;
 Query Match 62.9%; Score 70.5; DB 20; Length 37;
 Best Local Similarity 62.5%; Pred. No. 3.3e-06;
 Matches 20; Conservative 0; Mismatches 11; Indels 1; Gaps 1;
 QY 4 GTXXXXXKQEEAVRLXXXXL-XGXSXSGA 34
 DB 4 GTFTSDASKQMEBAVRLFIEMLKXGXSXSGA 35
 RESULT 14
 AAY24853
 ID AAY24853 standard; peptide; 37 AA.
 AC AAY24853;
 DT 24-AUG-1999 (first entry)
 DE Extendin agonist peptide #45.
 KM Extendin agonist; Heloderma sp.; Gila monster; venom; lizard;
 KM diabetes mellitus type I; diabetes mellitus type II; hyperglycaemia;
 KM hypoglycaemia; plasma glucose; gastric emptying; stomach emptying.
 OS Synthetic.
 OS Heloderma sp.
 PN W09925727-A2.
 PD 27-MAY-1999.
 PF 13-NOV-1998; 98MO-US24210.
 PR 14-NOV-1997; 97US-0065442.
 PA (AMYL-) AMYLIN PHARM INC.
 PI Beley NRA, Prickett KS;
 DR WPI; 1999-394773/33.
 XX PT New extendin agonist peptides - can regulate gastric motility and
 XX PT slow gastric emptying, used for treating, e.g. diabetes
 PS Claim 18; Fig 4; 108bp; English.
 CC AAY24809 to AAY24877 represent extendin agonist peptides which can
 CC regulate gastric motility and slow gastric emptying. The peptides can be
 CC used for treating e.g. diabetes or hyperglycaemic or hypoglycaemic
 CC conditions. The peptides are extendin agonists which have activity as
 CC agents to regulate gastric motility and to slow gastric emptying, as

CC evidenced by the ability to reduce post-prandial glucose levels in
 CC mammals. They can be used for the treatment of Type I and II diabetes and
 CC hyperglycaemic or hypoglycaemic conditions. They can also be used for the
 CC treatment of disorders which would be benefited by agents which lower
 CC plasma glucose levels and in treatment of disorders which would be
 CC benefited with agents useful in delaying and/or slowing gastric
 CC emptying.
 SQ Sequence 37 AA;
 Query Match 62.9%; Score 70.5; DB 20; Length 37;
 Best Local Similarity 59.4%; Pred. No. 3.3e-06;
 Matches 19; Conservative 0; Mismatches 12; Indels 1; Gaps 1;
 QY 4 GTXXXXXKQEEAVRLXXXXL-XGXSXSGA 34
 DB 4 GTFTSDASKQMEBAVRLFIEMLKXGXSXSGA 35
 RESULT 15
 AAY24854
 ID AAY24854 standard; peptide; 37 AA.
 AC AAY24854;
 DT 24-AUG-1999 (first entry)
 DE Extendin agonist peptide #46.
 KM Extendin agonist; Heloderma sp.; Gila monster; venom; lizard;
 KM diabetes mellitus type I; diabetes mellitus type II; hyperglycaemia;
 KM hypoglycaemia; plasma glucose; gastric emptying; stomach emptying.
 OS Synthetic.
 OS Heloderma sp.
 PN W09925727-A2.
 PD 27-MAY-1999.
 PF 13-NOV-1998; 98MO-US24210.
 PR 14-NOV-1997; 97US-0065442.
 PA (AMYL-) AMYLIN PHARM INC.
 PI Beley NRA, Prickett KS;
 DR WPI; 1999-394773/33.
 XX PT New extendin agonist peptides - can regulate gastric motility and
 XX PT slow gastric emptying, used for treating, e.g. diabetes
 PS Claim 18; Fig 4; 108bp; English.
 CC AAY24809 to AAY24877 represent extendin agonist peptides which can
 CC regulate gastric motility and slow gastric emptying. The peptides can be
 CC used for treating e.g. diabetes or hyperglycaemic or hypoglycaemic
 CC conditions. The peptides are extendin agonists which have activity as
 CC agents to regulate gastric motility and to slow gastric emptying, as
 CC evidenced by the ability to reduce post-prandial glucose levels in
 CC mammals. They can be used for the treatment of Type I and II diabetes and
 CC hyperglycaemic or hypoglycaemic conditions. They can also be used for the
 CC treatment of disorders which would be benefited by agents which lower
 CC plasma glucose levels and in treatment of disorders which would be
 CC benefited with agents useful in delaying and/or slowing gastric
 CC emptying.
 SQ Sequence 37 AA;
 Query Match 62.9%; Score 70.5; DB 20; Length 37;
 Best Local Similarity 59.4%; Pred. No. 3.3e-06;
 Matches 19; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

QY 4 GTXXXXXSKQXEEAVRLXXXXL-XGXSXSGA 34
 DB 4 GTFTSLSKQMEAEAVRLFIEWLKNXGXSXSGA 35

RESULT 16

AAB11275
 ID AAB11275 standard; Peptide: 37 AA.

AC AAB11275;

DT 20-FEB-2001 (first entry)

DE extendin agonist peptide SEQ ID NO 183.

KM Extendin; agonist; treatment; antidiabetic; insulin sensitivity; diabetes;

KX plasma glucose; gastric emptying; food intake.

OS Synthetic.

PN WO200041546-A2.

PD 20-JUL-2000.

PF 10-JAN-2000; 2000US-0116380.

PR 14-JAN-1999; 99US-0116380.

PA (AMYL-) AMYLIN PHARM INC.

PI Young A, L'italien JT, Kolterman O;

DR WPI; 2000-514584/46.

PT New formulations comprising an extendin or extendin agonist peptide used

PT for increasing the sensitivity of a subject to insulin to treat

PT diabetes -

PS Example 192; Page 238; 281pp; English.

XX This invention describes a novel formulation (I) comprising an extendin or

CC extendin agonist peptide, a buffer and an iso-osmolality modifier which

CC has a pH of 3-7. The products of the invention have antidiabetic

CC activity. The extendin or extendin agonist is used to increase the

CC sensitivity of a subject to insulin to treat diabetes and disorders which

CC would benefit from agents which lower plasma glucose levels and disorders

CC which would benefit from agents that delay and/or slow gastric emptying

CC or reducing food intake.

CC Sequence 37 AA;

QY Query Match 62.9%; Score 70.5; DB 21; Length 37;

DB Best Local Similarity 62.5%; Pred. No. 3.3e-06;

Matches 20; Conservative 0; Mismatches 11; Indels 1; Gaps 1;

QY 4 GTXXXXXSKQXEEAVRLXXXXL-XGXSXSGA 34

DB 4 GTFTSLSKQMEAEAVRLFIEWLKNXGXSXSGA 35

RESULT 17

AAB53041

ID AAB53041 standard; Peptide: 37 AA.

AC AAB53041;

DT 28-FEB-2001 (first entry)

DE Extendin agonist compound #169.

KM Extendin; agonist; diabetes; obesity; eating disorder;

KX dyslipidaemia; insulin-resistance syndrome; food intake.

XX Heloderma sp.

OS WO200066623-A1.

PN 09-NOV-2000.

PD 28-APR-2000; 2000WO-US11814.

PF 30-APR-1999; 99US-0132018.

PR (AMYL-) AMYLIN PHARM INC.

PA Young A, Prickett K;

PI WPI; 2000-672834/65.

DR Modified extendin or an extendin agonist linked to one or more

PT polyethylene glycol (PEG) polymers, modulate plasma glucose levels,

PT useful for treating disorders such as diabetes and obesity -

PS Disclosure; Fig 4; 119pp; English.

XX The present invention relates to extendins and their agonists which have

CC been modified with molecular weight increasing agents such as

CC polyethylene glycol (PEG). These can be used in the treatment of

CC diabetes, obesity, impaired glucose tolerance, postprandial dumping

CC syndrome, postprandial hyperglycaemia, eating disorders, insulin

CC resistance syndrome, dyslipidaemia and to suppress glucagon secretion.

CC Sequence 37 AA;

QY Query Match 62.9%; Score 70.5; DB 21; Length 37;

DB Best Local Similarity 62.5%; Pred. No. 3.3e-06;

Matches 20; Conservative 0; Mismatches 11; Indels 1; Gaps 1;

QY 4 GTXXXXXSKQXEEAVRLXXXXL-XGXSXSGA 34

DB 4 GTFTSLSKQMEAEAVRLFIEWLKNXGXSXSGA 35

RESULT 18

AA94196

ID AA94196 standard; peptide: 37 AA.

AC AA94196;

DT 20-OCT-2000 (first entry)

DE Amino acid sequence of an extendin agonist.

XX Extendin; Gila monster lizard; Mexican Beaded lizard; agonist;

XX glucagon-like peptide; plasma glucagon; necrolytic erythema;

XX glucagonoma; hyperglucagonemia; diabetes.

OS Synthetic.

OS Heloderma sp.

FT Key

FT Modified-site 31 Location/Qualifiers

FT Modified-site 36 /note= "N-methyl alanine"

FT Modified-site 37 /note= "N-methyl alanine"

FT Modified-site 38 /note= "N-methyl alanine"

FT Modified-site 38 /note= "amidated N-methyl alanine"

PN WO200041548-A2.

PD 20-JUL-2000.

PR 14-JAN-2000; 2000WO-US00942.

XX	14-JAN-1999;	99US-0116380.
PR	30-APR-1999;	99US-0132017.
PR	10-JAN-2000;	2000US-0175365.
XX	(AMYL-) AMYLIN PHARM INC.	
PA	Young A, Gedulin B;	
PI	WPI; 2000-490999/43.	
XX		
DR	Lowering plasma glucagon using exendin, an exendin agonist, a modified	
PT	exendin or a modified exendin agonist, useful for treating	
PT	hyperglucagonemia and diabetes -	
XX	Disclosure, Fig 4G; 96pp; English.	
PS		
XX	The present sequence represents a modified exendin or exendin agonist.	
XX	Exendins are found in the salivary glands of the Gila monster and	
CC	Mexican Beaded lizard, and have sequence similarity to glucagon-like	
CC	peptides. They are used in the method of the invention. The specification	
CC	describes a method for lowering plasma glucagon, comprising administering	
CC	an exendin, an exendin agonist, a modified exendin or a modified exendin	
CC	agonist. These compounds lower plasma glucagon level. The method is	
CC	useful for lowering plasma glucagon in subjects, preferably humans,	
CC	suffering from neorolytic erythema or glucagonoma. The method is also	
CC	useful for treating hyperglucagonemia and other conditions that would	
CC	benefit from reduced glucagon levels and/or suppression of glucagon,	
CC	e.g. type 1 and type 2 diabetes.	
XX		
SQ	Sequence 37 AA;	
Query Match	62.9%; Score 70.5; DB 21; Length 37;	
Best Local Similarity	62.5%; Pred. No. 3,3e-06;	
Matches 20; Conservative 0; Mismatches 11; Indels 1; Gaps 1		
QY	4 GTXXXXXSKQEEEAARLXXXXL-XGGXSSGA 34	
DB	4 GTTSAISKQEEEAARLFIETWLRKGGXSSGA 35	
RESULT 19		
AAE08427		
ID	AAE08427 standard; peptide; 37 AA.	
XX	AAE08427;	
AC		
XX	01-NOV-2001 (First entry)	
DT		
XX	Exendin agonist peptide #72.	
DE		
XX	Exendin agonist; antilipemic; cardiact; triglyceride; inotropic;	
XX	diuretic; coronary heart disease; dyslipidaemia.	
KW		
XX	Synthetic.	
XX		
FH	Key	Location/Qualifiers
FT	Modified-site	31
FT	Modified-site	/note= "N-Methyl-alanine"
FT	Modified-site	37
FT	Modified-site	/note= "C-terminal amide"
XX		
XX	WO200151078-A1.	
PN		
XX	19-JUL-2001.	
PD		
XX	09-JAN-2001; 2001WO-US00719.	
PF		
XX	10-JAN-2000; 2000US-0175365.	
PR		
XX	(AMYL-) AMYLIN PHARM INC.	
PA		
XX	Kolterman OG, Young AA;	
XX		

XX	WP1: 2001-514422/56.
DR	
XX	
PT	Use of extendin and extendin agonist compounds for modulating
PT	triglyceride levels, and treating heart disease and dyslipidemia
XX	
PS	Example 76; Page 82; 16pp; English.
XX	
CC	The patent discloses a method for modulating plasma or postprandial
CC	triglyceride and other lipid levels by administering extendin or an
CC	extendin agonist. Extendins have inotropic and diuretic effects. They
CC	suppress the secretion of glucagon. Extendin and its agonists have
CC	a significant effect on the reduction of blood serum triglyceride
CC	concentrations. They are used to treat coronary heart disease and
CC	dyslipidaemia, and for modifying postprandial triglyceride levels.
CC	The present peptide sequence is an agonist of extendin.
SQ	
SQ	Sequence 37 AA;
Query Match	62.9%; Score 70.5; DB 22; Length 37;
Beet Local Similarity	59.4%; Pred. No. 3.3e-06;
Matches	19; Conservative 0; Mismatches 12; Indels 1; Gaps 1
Dy	
Dy	4 GTXXXXXSKQXEBAVRLXXXXL-XGXSSGA 34
Dy	4 GTFTSDLSKQMEBEAVRLFIEWLKNKGSSGA 35
ID	
AAE08428	
AAE08428	standard; peptide; 37 AA.
AC	
AAE08428;	
DT	01-NOV-2001 (first entry)
DE	
DE	Extendin agonist peptide #73.
KM	Exendin agonist; antilipemic; cardiac; triglyceride; inotropic;
KW	diuretic; coronary heart disease; dyslipidaemia.
OS	Synthetic.
Key	Location/Qualifiers
Modified-site	31 /note= "N-Methyl-alanine"
Modified-site	36 /note= "N-Methyl-alanine"
Modified-site	37 /note= "N-Methyl-alanine; C-terminal amide"
WO200151078-A1.	
19-JUL-2001.	
09-JAN-2001; 2001WC-US00719.	
10-JAN-2000; 2000US-0175365.	
(AMYL-) AMYLIN PHARM INC.	
Kolterman OG, Young AA;	
WP1: 2001-514422/56.	
The patent discloses a method for modulating plasma or postprandial	
triglyceride and other lipid levels by administering extendin or an	
extendin agonist. Extendins have inotropic and diuretic effects. They	
suppress the secretion of glucagon. Extendin and its agonists have	
a significant effect on the reduction of blood serum triglyceride	
concentrations. They are used to treat coronary heart disease and	
dyslipidaemia, and for modifying postprandial triglyceride levels.	
The present peptide sequence is an agonist of extendin.	

CC suppress the secretion of glucagon. Exendin and its agonists have
CC a significant effect on the reduction of blood serum triglyceride
CC concentrations. They are used to treat coronary heart disease and
CC dyslipidaemia, and for modifying postprandial triglyceride levels.
CC The present peptide sequence is an agonist of exendin.

XX
SQ Sequence 37 AA;

Query Match 62.9%; Score 70.5; DB 22; Length 37;
Best Local Similarity 59.4%; Pred. No. 3.3e-06;
Matches 19; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

OY 4 GTXXXXXSKQEEAVRLXXXXL-XGXSXSGA 34
4 GTFTSDLSKQMEAEAVRLFIEMLNKQXSXSGA 35

RESULT 21
AAE08443
ID AAE08443 standard; peptide: 37 AA.

XX AAE08443;
XX
XX 01-NOV-2001 (first entry)

XX Exendin agonist peptide #88.

XX Exendin agonist; antilipemic; cardiac; triglyceride; inotropic;
KM diuretic; coronary heart disease; dyslipidaemia.

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 31 /note= "Homoproline"

FT Modified-site 36 /note= "Homoproline"

FT Modified-site 37 /note= "Homoproline"

XX W0200151078-A1.

XX 19-JUL-2001.

XX 09-JAN-2001; 2001WO-US00719.

XX 10-JAN-2000; 2000US-0175365.

XX (AMYL-) AMYLIN PHARM INC.

XX Kolterman OG, Young AA;

XX WPI, 2001-514422/56.

XX Use of exendin and exendin agonist compounds for modulating

XX triglyceride levels, and treating heart disease and dyslipidaemia

XX Example 92; Page 92; 161pp; English.

XX The patent discloses a method for modulating plasma or postprandial
CC triglyceride and other lipid levels by administering exendin or an
CC exendin agonist. Exendins have inotropic and diuretic effects. They
CC suppress the secretion of glucagon. Exendin and its agonists have
CC a significant effect on the reduction of blood serum triglyceride
CC concentrations. They are used to treat coronary heart disease and
CC dyslipidaemia, and for modifying postprandial triglyceride levels.
CC The present peptide sequence is an agonist of exendin.

XX
SQ Sequence 37 AA;

Query Match 62.9%; Score 70.5; DB 22; Length 37;
Best Local Similarity 59.4%; Pred. No. 3.3e-06;
Matches 20; Conservative 0; Mismatches 11; Indels 1; Gaps 1;

OY 4 GTXXXXXSKQEEAVRLXXXXL-XGXSXSGA 34
4 GTFTSDLSKQMEAEAVRLFIEMLNKQXSXSGA 35

RESULT 22
AAB64263

ID AAB64263 standard; peptide: 37 AA.

XX AAB64263;

XX 27-MAR-2001 (first entry)

XX Exendin agonist, SEQ ID NO:83.

XX Exendin agonist; gestational diabetes mellitus; GDM; insulin resistance;
KM pregnancy complication; neonatal abnormality; blood glucose modulator;
KM insulinotropic; anorectic; exendin-4.

XX Heloderma suspectum.

XX Synthetic.

XX W0200073331-A2.

XX 07-DEC-2000.

XX 23-MAY-2000; 2000WO-US14231.

XX 01-JUN-1999; 99US-0323867.

XX (AMYL-) AMYLIN PHARM INC.

XX Hiles R, Prickett KS;

XX WPI, 2001-137634/14.

XX Use of exendins or exendin agonists for lowering or reducing blood

XX glucose levels and treating gestational diabetes mellitus in a subject,

XX especially in a human -

XX Example 76; Page 67; 133pp; English.

XX The invention relates to the use of an exendin (AAB64181-B64182) or
CC an exendin agonist (AAB64185-B64368) for treating gestational diabetes
CC mellitus (GDM) in a patient. GDM arises during pregnancy, and is due
CC to a combination of increased insulin resistance and a diminished
CC ability to increase insulin secretion. In contrast, in a normal
CC pregnancy, both insulin resistance and insulin secretion increase. GDM
CC pregnancies are associated with complications in both the mother and the
CC fetus. Women with GDM have increased rates of Caesarian delivery,
CC hypertensive disorders such as pre-eclampsia, and urinary tract
CC infections. GDM results in an elevated rate of foetal abnormalities such
CC as neural tube defects, and is associated with an increased risk of
CC neonatal morbidities such as hypoglycaemia, hypocalcaemia,
CC hypomagnesaemia, polycythaemia, hyperbilirubinaemia, and subsequent
CC childhood and adolescent obesity. Exendins are peptides from the salivary
CC secretions of the Gila monster (exendin-4) and the Mexican bearded lizard
CC (exendin-3) which exhibit homology with several members of the
CC glucagon-like peptide family, particularly GLP-1, and have similar
CC insulinotropic effects. Unlike the compounds used to treat type 2
CC diabetes, which are contraindicated for GDM, exendins and exendin
CC agonists do not cross the placenta and thus do not cause severe prolonged
CC hypoglycaemia in the newborn. They have a potent and prolonged effect on
CC blood glucose, and, unlike conventional insulin therapy, should not cause
CC weight gain, as they inhibit gastric emptying and reduce appetite. The
CC present sequence represents an exendin agonist of the invention which is
CC based upon the sequence of exendin-4.

XX
SQ Sequence 37 AA;

Query Match 62.9%; Score 70.5; DB 22; Length 37;
Best Local Similarity 59.4%; Pred. No. 3.3e-06;

Matches 19; Conservative 0; Mismatches 12; Indels 1; Gaps 1;
QY 4 GTXXXXXKQXEEAVRLXXXXL-XGXSXSGA 34
Db 4 GTFTSDLSKQMEEAVALRFLIEWLKNKGASXSGA 35

RESULT 23

AAB64264 AAB64264 standard; peptide; 37 AA.

XX AAB64264;

XX 27-MAR-2001 (first entry)

XX Extendin agonist, SEQ ID NO:84.

XX Extendin agonist; gestational diabetes mellitus; GDM; insulin resistance;
KM pregnancy complication; neonatal abnormality; blood glucose modulator;
KM insulinotropic; anorectic; extendin-4.

XX Heloderma suspectum.
OS Synthetic.

XX WO200073331-A2.

XX 07-DEC-2000.

XX 23-MAY-2000; 2000WO-US14231.

XX 01-JUN-1999; 99US-0323867.

XX (AMYL-) AMYLIN PHARM INC.

XX Hiles R, Prickett KS;

XX WPI; 2001-137634/14.

XX Use of extendins or extendin agonists for lowering or reducing blood
PT glucose levels and treating gestational diabetes mellitus in a subject,
PT especially in a human -
XX

PS Example 77; Page 68; 133pp; English.

XX The invention relates to the use of an extendin (AAB64181-B64182) or
CC an extendin agonist (AAB64185-B64368) for treating gestational diabetes
CC mellitus (GDM) in a patient. GDM arises during pregnancy, and is due
CC to a combination of increased insulin resistance and a diminished
CC ability to increase insulin secretion. In contrast, in a normal
CC pregnancy, both insulin resistance and insulin secretion increase. GDM
CC pregnancies are associated with complications in both the mother and the
CC foetus. Women with GDM have increased rates of Caesarian delivery,
CC hypertensive disorders such as pre-eclampsia, and urinary tract
CC infections. GDM results in an elevated rate of foetal abnormalities such
CC as neural tube defects, and is associated with an increased risk of
CC neonatal morbidities such as hypoglycaemia, hypocalcaemia, and
CC hypomagnesaemia, polycythaemia, hyperbilirubinaemia, and subsequent
CC childhood and adolescent obesity. Extendins are peptides from the salivary
CC secretions of the Gila monster (extendin-4) and the Mexican beaded lizard
CC (extendin-3) which exhibit homology with several members of the
CC glucagon-like peptide family, particularly GLP-1, and have similar
CC insulinotropic effects. Unlike the compounds used to treat type 2
CC diabetes, which are contraindicated for GDM, extendins and extendin
CC agonists do not cross the placenta and thus do not cause severe prolonged
CC hypoglycaemia in the newborn. They have a potent and prolonged effect on
CC blood glucose, and, unlike conventional insulin therapy, should not cause
CC weight gain, as they inhibit gastric emptying and reduce appetite. The
CC present sequence represents an extendin agonist of the invention which is
CC based upon the sequence of extendin-4.

XX Sequence 37 AA;

SQ Query Match

62.9%; Score 70.5; DB 22; Length 37;

Best Local Similarity 59.4%; Pred. No. 3.3e-06;
Matches 19; Conservative 0; Mismatches 12; Indels 1; Gaps 1;
QY 4 GTXXXXXKQXEEAVRLXXXXL-XGXSXSGA 34
Db 4 GTFTSDLSKQMEEAVALRFLIEWLKNKGASXSGA 35

RESULT 24

AAB64279 AAB64279 standard; peptide; 37 AA.

XX AAB64279;

XX 27-MAR-2001 (first entry)

XX Extendin agonist, SEQ ID NO:99.

XX Extendin agonist; gestational diabetes mellitus; GDM; insulin resistance;
KM pregnancy complication; neonatal abnormality; blood glucose modulator;
KM insulinotropic; anorectic; extendin-4.

XX Heloderma suspectum.
OS Synthetic.

XX WO200073331-A2.

XX 07-DEC-2000.

XX 23-MAY-2000; 2000WO-US14231.

XX 01-JUN-1999; 99US-0323867.

XX (AMYL-) AMYLIN PHARM INC.

XX Hiles R, Prickett KS;

XX WPI; 2001-137634/14.

XX Use of extendins or extendin agonists for lowering or reducing blood
PT glucose levels and treating gestational diabetes mellitus in a subject,
PT especially in a human -
XX

PS Example 92; Page 75; 133pp; English.

XX The invention relates to the use of an extendin (AAB64181-B64182) or
CC an extendin agonist (AAB64185-B64368) for treating gestational diabetes
CC mellitus (GDM) in a patient. GDM arises during pregnancy, and is due
CC to a combination of increased insulin resistance and a diminished
CC ability to increase insulin secretion. In contrast, in a normal
CC pregnancy, both insulin resistance and insulin secretion increase. GDM
CC pregnancies are associated with complications in both the mother and the
CC foetus. Women with GDM have increased rates of Caesarian delivery,
CC hypertensive disorders such as pre-eclampsia, and urinary tract
CC infections. GDM results in an elevated rate of foetal abnormalities such
CC as neural tube defects, and is associated with an increased risk of
CC neonatal morbidities such as hypoglycaemia, hypocalcaemia, and
CC hypomagnesaemia, polycythaemia, hyperbilirubinaemia, and subsequent
CC childhood and adolescent obesity. Extendins are peptides from the salivary
CC secretions of the Gila monster (extendin-4) and the Mexican beaded lizard
CC (extendin-3) which exhibit homology with several members of the
CC glucagon-like peptide family, particularly GLP-1, and have similar
CC insulinotropic effects. Unlike the compounds used to treat type 2
CC diabetes, which are contraindicated for GDM, extendins and extendin
CC agonists do not cross the placenta and thus do not cause severe prolonged
CC hypoglycaemia in the newborn. They have a potent and prolonged effect on
CC blood glucose, and, unlike conventional insulin therapy, should not cause
CC weight gain, as they inhibit gastric emptying and reduce appetite. The
CC present sequence represents an extendin agonist of the invention which is
CC based upon the sequence of extendin-4.

XX Sequence 37 AA;

SQ

Query Match 62.9%; Score 70.5; DB 22; Length 37;
 Best Local Similarity 62.5%; Pred. No. 3.3e-06;
 Matches 20; Conservative 0; Mismatches 11; Indels 1; Gaps 1;

4 GTXXXXXSKXEEFAVRLXXXXL-XGXSXSGA 34
 4 GTFTSDLSKXMEFAVRLFTFWLKNKGXSSGA 35

RESULT 25

AA11311 standard; Peptide; 39 AA.

AA11311;
 20-FEB-2001 (first entry)

exendin agonist peptide SEQ ID NO 37.

Exendin; agonist; treatment; antidiabetic; insulin sensitivity; diabetes;
 plasma glucose; gastric emptying; food intake.

Synthetic.

MO200041546-A2.

10-JAN-2000; 2000US-0116380.

14-JAN-1999; 99US-0116380.

(AMYL-) AMYLIN PHARM INC.

Young A, L'Italian JJ, Koltzman O;

WPI; 2000-514564/46.

New formulations comprising an exendin or exendin agonist peptide used

for increasing the sensitivity of a subject to insulin to treat

diabetes -

Example 42; Figure 15; 281pp; English.

This invention describes a novel formulation (I) comprising an exendin or

exendin agonist peptide, a buffer and an iso-osmolality modifier which

has a pH of 3-7. The products of the invention have antidiabetic

activity. The exendin or exendin agonist is used to increase the

sensitivity of a subject to insulin to treat diabetes and disorders which

would benefit from agents which lower plasma glucose levels and disorders

CC which would benefit from agents that delay and/or slow gastric emptying

or reducing food intake.

Sequence 39 AA;

Query Match 62.9%; Score 70.5; DB 21; Length 39;

Best Local Similarity 59.4%; Pred. No. 3.5e-06;

Matches 19; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

4 GTXXXXXSKXEEFAVRLXXXXL-XGXSXSGA 34

4 GTFTSDLSKXMEFAVRLFTFWLKNKGXSSGA 35

RESULT 26

AA194039 standard; peptide; 39 AA.

AA194039;

20-OCT-2000 (first entry)

Amino acid sequence of an exendin agonist.

Exendin; Gila monster lizard; Mexican Beaded lizard; agonist;
 glucagon-like peptide; plasma glucagon; necrolytic erythema;
 glucagonoma; hyperglucagonemia; diabetes.

Synthetic.

Heloderma sp.

Key Location/Qualifiers

Modified-site 31 /note= "thioprolin"

Modified-site 36 /note= "thioprolin"

Modified-site 37 /note= "thioprolin"

Modified-site 38 /note= "thioprolin"

MO200041548-A2.

14-JAN-2000; 2000MO-US00942.

14-JAN-1999; 99US-0116380.

30-APR-1999; 99US-0132017.

10-JAN-2000; 2000US-0175365.

(AMYL-) AMYLIN PHARM INC.

Young A, Gedulin B;

WPI; 2000-490999/43.

Lowering plasma glucagon using exendin, an exendin agonist, a modified

exendin or a modified exendin agonist, useful for treating

hyperglucagonemia and diabetes -

Disclosure; Fig 3B; 96pp; English.

AA194013-43 represent exendin agonists, derived from AA194012.

CC Extending are found in the salivary glands of the Gila monster and

CC Mexican Beaded lizard, and have sequence similarity to glucagon-like

CC peptides. They are used in the method of the invention. The specification

CC describes a method for lowering plasma glucagon, comprising administering

CC an exendin, an exendin agonist, a modified exendin or a modified exendin

CC agonist. These compounds lower plasma glucagon level. The method is

CC useful for lowering plasma glucagon in subjects, preferably humans,

CC suffering from necrolytic erythema or glucagonoma. The method is also

CC useful for treating hyperglucagonemia and other conditions that would

CC benefit from reduced glucagon levels and/or suppression of glucagon,

CC e.g. type 1 and type 2 diabetes.

Sequence 39 AA;

Query Match 62.9%; Score 70.5; DB 21; Length 39;

Best Local Similarity 62.5%; Pred. No. 3.5e-06;

Matches 20; Conservative 0; Mismatches 11; Indels 1; Gaps 1;

4 GTXXXXXSKXEEFAVRLXXXXL-XGXSXSGA 34

4 GTFTSDLSKXMEFAVRLFTFWLKNKGXSSGA 35

RESULT 27

AA194040 standard; peptide; 39 AA.

AA194040;

20-OCT-2000 (first entry)

Amino acid sequence of an exendin agonist.

XX	Extending; Gila monster lizard; Mexican Beaded lizard; agonist;
KM	glucagon-like peptide; plasma glucagon; necrolytic erythema;
KM	glucagonoma; hyperglucagonemia; diabetes.
XX	
OS	Synthetic.
XX	Heloderma sp.
FH	
FT	Key Location/Qualifiers
FT	Modified-site 31
FT	/note= "homoproline"
FT	Modified-site 36
FT	/note= "homoproline"
FT	Modified-site 37
FT	/note= "homoproline"
FT	Modified-site 38
FT	/note= "homoproline"
PN	WO200041548-A2.
XX	
PD	20-UTL-2000.
PF	14-JAN-2000; 200OWO-US00942.
PR	14-JAN-1999; 99US-0116380.
PR	30-APR-1999; 99US-0132017.
PR	10-JAN-2000; 200OUS-0175365.
XX	
PA	(AMYL-) AMYLIN PHARM INC.
XX	
PI	Young A, Gedulin B;
XX	
DR	WPI; 2000-490999/43.
PT	Lowering plasma glucagon using extendin, an extendin agonist, a modified
PT	extendin or a modified extendin agonist, useful for treating
XT	hyperglucagonemia and diabetes -
XX	
PS	Disclosure; Fig 3B; 96pp; English.
XX	
CC	AA94013-43 represent extendin agonists, derived from AA94012.
CC	Extendins are found in the salivary glands of the Gila monster and
CC	Mexican Beaded lizard, and have sequence similarity to glucagon-like
CC	peptides. They are used in the method of the invention. The specification
CC	describes a method for lowering plasma glucagon comprising administering
CC	an extendin, an extendin agonist, a modified extendin or a modified extendin
CC	agonist. These compounds lower plasma glucagon level. The method is
CC	useful for lowering plasma glucagon in subjects, preferably humans,
CC	suffering from neolytic erythema or glucagonoma. The method is also
CC	benefit for treating hyperglucagonemia and other conditions that would
CC	e.g. type 1 and type 2 diabetes.
XX	
SQ	Sequence 39 AA:
OY	Query Match 62.9%; Score 70.5; DB 21; Length 39;
DB	Best Local Similarity 62.5%; Pred. No. 3.5e-06;
	Matches 20; Conservative 0; Mismatches 11; Indels 1; Gaps 1
	4 GTXXXXXSKOXEEAVRLXXXXL-XGGXS SGA 34
	4 GTFTDLSKQLEFEAVRLFIEFLKNKGXS SGA 35
RESULT 28	
ID	AA94043 standard; peptide; 39 AA.
AC	AA94043;
DT	20-OCT-2000 (first entry)
DE	Amino acid sequence of an extendin agonist.

Query Match	62.9%	Score 70.5	DB 21	Length 39
Best Local Similarity	62.5%	Pred. 0.35e-06		
Matches 20	Conservative 0	Mismatches 11	Indels 1	Gaps 1
4 GTXXXXXXSKKEFAVRLXXXXL-XGGXSSGA 34				
4 GTFTSDLSKQLEERAVRLFTEFLNKGXSSGA 35				
Sequence 39 AA:				
AAV94013-43 represent extendin agonists, derived from AAV94012.				
Extendins are found in the salivary glands of the Gila monster and Mexican Beaded lizard, and have sequence similarity to glucagon-like peptides. They are used in the method of the invention. The specification describes a method for lowering plasma glucagon, comprising administering an extendin, an extendin agonist, a modified extendin or a modified extendin agonist. These compounds lower plasma glucagon level. The method is useful for lowering plasma glucagon in subjects, preferably humans, suffering from necrolytic erythema or glucagonoma. The method is also useful for treating hyperglycemic glucagonemia and other conditions that would benefit from reduced glucagon levels and/or suppression of glucagon, e.g. type 1 and type 2 diabetes.				
Disclosure, Fig 3B, 96pp; English.				
14-JAN-1999; 99US-0116380.				
30-APR-1999; 99US-0132017.				
10-JAN-2000; 2000US-0175365.				
(AMYL-) AMYLIN PHARM INC.				
Young A, Gedulin B,				
WPI; 2000-490599/43.				
Lowering plasma glucagon using extendin, an extendin agonist, a modified extendin or a modified extendin agonist, useful for treating hyperglycemic glucagonemia and diabetes -				
Disclosure, Fig 3B, 96pp; English.				
14-JAN-1999; 99US-0116380.				
30-APR-1999; 99US-0132017.				
10-JAN-2000; 2000US-0175365.				
(AMYL-) AMYLIN PHARM INC.				
Young A, Gedulin B,				
WPI; 2000-490599/43.				
Lowering plasma glucagon using extendin, an extendin agonist, a modified extendin or a modified extendin agonist, useful for treating hyperglycemic glucagonemia and diabetes -				
Disclosure, Fig 3B, 96pp; English.				
14-JAN-1999; 99US-0116380.				
30-APR-1999; 99US-0132017.				
10-JAN-2000; 2000US-0175365.				
(AMYL-) AMYLIN PHARM INC.				
Young A, Gedulin B,				
WPI; 2000-490599/43.				
Lowering plasma glucagon using extendin, an extendin agonist, a modified extendin or a modified extendin agonist, useful for treating hyperglycemic glucagonemia and diabetes -				
Disclosure, Fig 3B, 96pp; English.				
14-JAN-1999; 99US-0116380.				
30-APR-1999; 99US-0132017.				
10-JAN-2000; 2000US-0175365.				
(AMYL-) AMYLIN PHARM INC.				
Young A, Gedulin B,				
WPI; 2000-490599/43.				
Lowering plasma glucagon using extendin, an extendin agonist, a modified extendin or a modified extendin agonist, useful for treating hyperglycemic glucagonemia and diabetes -				
Disclosure, Fig 3B, 96pp; English.				
14-JAN-1999; 99US-0116380.				
30-APR-1999; 99US-0132017.				
10-JAN-2000; 2000US-0175365.				
(AMYL-) AMYLIN PHARM INC.				
Young A, Gedulin B,				
WPI; 2000-490599/43.				
Lowering plasma glucagon using extendin, an extendin agonist, a modified extendin or a modified extendin agonist, useful for treating hyperglycemic glucagonemia and diabetes -				
Disclosure, Fig 3B, 96pp; English.				
14-JAN-1999; 99US-0116380.				
30-APR-1999; 99US-0132017.				
10-JAN-2000; 2000US-0175365.				
(AMYL-) AMYLIN PHARM INC.				
Young A, Gedulin B,				
WPI; 2000-490599/43.				
Lowering plasma glucagon using extendin, an extendin agonist, a modified extendin or a modified extendin agonist, useful for treating hyperglycemic glucagonemia and diabetes -				
Disclosure, Fig 3B, 96pp; English.				
14-JAN-1999; 99US-0116380.				
30-APR-1999; 99US-0132017.				
10-JAN-2000; 2000US-0175365.				
(AMYL-) AMYLIN PHARM INC.				
Young A, Gedulin B,				
WPI; 2000-490599/43.				
Lowering plasma glucagon using extendin, an extendin agonist, a modified extendin or a modified extendin agonist, useful for treating hyperglycemic glucagonemia and diabetes -				
Disclosure, Fig 3B, 96pp; English.				
14-JAN-1999; 99US-0116380.				
30-APR-1999; 99US-0132017.				
10-JAN-2000; 2000US-0175365.				
(AMYL-) AMYLIN PHARM INC.				
Young A, Gedulin B,				
WPI; 2000-490599/43.				
Lowering plasma glucagon using extendin, an extendin agonist, a modified extendin or a modified extendin agonist, useful for treating hyperglycemic glucagonemia and diabetes -				
Disclosure, Fig 3B, 96pp; English.				
14-JAN-1999; 99US-0116380.				
30-APR-1999; 99US-0132017.				
10-JAN-20				

XX Exendin agonist; antilipemic; cardiast; triglyceride; inotropic;
KW diuretic; coronary heart disease; dyslipidaemia.
XX Synthetic.
OS
XX
FH Key Location/Qualifiers
FT Modified-site 31
FT Modified-site /note= "Thioprolone"
FT Modified-site 36
FT Modified-site /note= "Thioprolone"
FT Modified-site 37
FT Modified-site /note= "Thioprolone"
FT Modified-site 38
FT Modified-site /note= "Thioprolone"
FT Modified-site 39
FT Modified-site /note= "C-terminal amide"
FT
FT
XX WO200151078-A1.
XX
XX 19-JUL-2001.
XX
XX 09-JAN-2001; 2001WO-US00719.
XX
XX 10-JAN-2000; 2000US-0175365.
XX
XX (AMYL-) AMYLIN PHARM INC.
XX
XX Kolterman OG, Young AA;
XX
XX WPI; 2001-514422/56.
XX
XX
XX Use of exendin and exendin agonist compounds for modulating
PT triglyceride levels, and treating heart disease and dyslipidemia -
XX
XX
XX Example 26; Page -: 161pp; English.
XX
XX The patent discloses a method for modulating plasma or postprandial
CC triglyceride and other lipid levels by administering exendin or an
CC exendin agonist. Exendins have inotropic and diuretic effects. They
CC suppress the secretion of glucagon. Exendin and its agonists have
CC a significant effect on the reduction of blood serum triglyceride
CC concentrations. They are used to treat coronary heart disease and
CC dyslipidaemia, and for modifying postprandial triglyceride levels.
CC The present peptide sequence is an agonist of exendin.
CC Note: The present sequence is not shown in the specification but is
CC derived from SEQ ID NO:3 shown in page 17 of the specification.
CC
XX
SQ Sequence 39 AA;
Query Match 62.9%; Score 70.5; DB 22; Length 39;
Best Local Similarity 62.5%; Pred. No. 3.5e-06;
Matches 20; Conservative 0; Mismatches 11; Indels 1; Gaps 1;
QY 4 GTXXXXXSKQEEBAVRLXXXXL-XGXSSGA 34
DB 4 GFTSDLSKQLEBAVRLFIPLKXGXSSGA 35
RESULT 30
AAE08380
ID AAE08380 standard; peptide; 39 AA.
XX
XX AAE08380;
AC
XX
XX 01-NOV-2001 (first entry)
DT
XX
XX Exendin agonist peptide #27.
DE
XX
XX Exendin agonist; antilipemic; cardiast; triglyceride; inotropic;
KW diuretic; coronary heart disease; dyslipidaemia.
XX
OS Synthetic.

XX
FH Key Location/Qualifiers
FT Modified-site 31
FT Modified-site /note= "Homoprolone"
FT Modified-site 36
FT Modified-site /note= "Homoprolone"
FT Modified-site 37
FT Modified-site /note= "Homoprolone"
FT Modified-site 38
FT Modified-site /note= "Homoprolone"
FT Modified-site 39
FT Modified-site /note= "C-terminal amide"
FT
FT
XX WO200151078-A1.
XX
XX 19-JUL-2001.
XX
XX 09-JAN-2001; 2001WO-US00719.
XX
XX 10-JAN-2000; 2000US-0175365.
XX
XX (AMYL-) AMYLIN PHARM INC.
XX
XX Kolterman OG, Young AA;
XX
XX WPI; 2001-514422/56.
XX
XX
XX Example 27; Page -: 161pp; English.
XX
XX The patent discloses a method for modulating plasma or postprandial
CC triglyceride and other lipid levels by administering exendin or an
CC exendin agonist. Exendins have inotropic and diuretic effects. They
CC suppress the secretion of glucagon. Exendin and its agonists have
CC a significant effect on the reduction of blood serum triglyceride
CC concentrations. They are used to treat coronary heart disease and
CC dyslipidaemia, and for modifying postprandial triglyceride levels.
CC The present peptide sequence is an agonist of exendin.
CC Note: The present sequence is not shown in the specification but is
CC derived from SEQ ID NO:3 shown in page 17 of the specification.
CC
XX
SQ Sequence 39 AA;
Query Match 62.9%; Score 70.5; DB 22; Length 39;
Best Local Similarity 62.5%; Pred. No. 3.5e-06;
Matches 20; Conservative 0; Mismatches 11; Indels 1; Gaps 1;
QY 4 GTXXXXXSKQEEBAVRLXXXXL-XGXSSGA 34
DB 4 GFTSDLSKQLEBAVRLFIPLKXGXSSGA 35
Search completed: December 23, 2003, 10:01:24
Job time : 36.5 secs

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OM protein - protein search, using sw model

Run on: December 23, 2003, 09:59:56 / Search time 14.5 Seconds

(without alignments)
116.720 Million cell updates/sec

Title: US-09-889-331a-48

Perfect score: 112
Sequence: 1 XXXGTXXXXXKXEEAVRLXXXXLXGXSXSGAXXXXXX 40

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database: Issued Patents AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	70.5	62.9	36	4	US-09-323-867A-171
2	70.5	62.9	37	4	US-09-323-867A-99
3	70.5	62.9	37	4	US-09-323-867A-183
4	70.5	62.9	39	4	US-09-323-867A-15
5	70.5	62.9	39	4	US-09-323-867A-36
6	70.5	62.9	39	4	US-09-323-867A-39
7	69.5	62.1	35	4	US-09-323-867A-69
8	69.5	62.1	35	4	US-09-323-867A-173
9	69.5	62.1	36	4	US-09-323-867A-67
10	69.5	62.1	36	4	US-09-323-867A-86
11	69.5	62.1	36	4	US-09-323-867A-170
12	69.5	62.1	36	4	US-09-323-867A-184
13	69.5	62.1	37	4	US-09-323-867A-65
14	69.5	62.1	37	4	US-09-323-867A-83
15	69.5	62.1	37	4	US-09-323-867A-84
16	69.5	62.1	37	4	US-09-323-867A-85
17	69.5	62.1	38	4	US-09-323-867A-63
18	69.5	62.1	38	4	US-09-323-867A-81
19	69.5	62.1	38	4	US-09-323-867A-168
20	69.5	62.1	38	4	US-09-323-867A-181
21	69.5	62.1	39	4	US-09-323-867A-9
22	69.5	62.1	39	4	US-09-323-867A-11
23	69.5	62.1	39	4	US-09-323-867A-21
24	69.5	62.1	39	4	US-09-323-867A-23
25	69.5	62.1	39	4	US-09-323-867A-26
26	69.5	62.1	39	4	US-09-323-867A-28
27	69.5	62.1	39	4	US-09-323-867A-30

28	69.5	62.1	39	4	US-09-323-867A-31	Sequence 31, Appl
29	69.5	62.1	39	4	US-09-323-867A-33	Sequence 37, Appl
30	69.5	62.1	39	4	US-09-323-867A-37	Sequence 188, Appl
31	69.5	62.1	39	4	US-09-323-867A-168	Sequence 68, Appl
32	69.5	62.1	35	4	US-09-323-867A-87	Sequence 87, Appl
33	69.5	62.1	35	4	US-09-323-867A-172	Sequence 172, Appl
34	69.5	62.1	35	4	US-09-323-867A-185	Sequence 65, Appl
35	69.5	62.1	35	4	US-09-323-867A-165	Sequence 165, Appl
36	69.5	62.1	35	4	US-09-323-867A-167	Sequence 167, Appl
37	69.5	62.1	35	4	US-09-323-867A-132	Sequence 132, Appl
38	69.5	62.1	37	4	US-09-323-867A-64	Sequence 64, Appl
39	69.5	62.1	37	4	US-09-614-847-130	Sequence 130, Appl
40	69.5	62.1	37	4	US-09-614-847-140	Sequence 140, Appl
41	69.5	62.1	38	4	US-09-323-867A-62	Sequence 62, Appl
42	69.5	62.1	38	4	US-09-323-867A-82	Sequence 82, Appl
43	69.5	62.1	38	4	US-09-323-867A-167	Sequence 167, Appl
44	69.5	62.1	38	4	US-09-614-847-101	Sequence 101, Appl
45	69.5	62.1	38	4	US-09-614-847-104	Sequence 104, Appl
46	69.5	62.1	38	4	US-09-614-847-129	Sequence 129, Appl
47	69.5	62.1	39	1	US-08-066-480-1	Sequence 1, Appl
48	69.5	62.1	39	1	US-08-066-480-2	Sequence 2, Appl
49	69.5	62.1	39	3	US-09-302-596-7	Sequence 7, Appl
50	69.5	62.1	39	3	US-09-302-596-9	Sequence 9, Appl

ALIGNMENTS

```

RESULT 1
US-09-323-867A-171
; Sequence 171, Application US/09323867A
; Patent No. 6506724
; GENERAL INFORMATION:
; APPLICANT: Amylin Pharmaceuticals, Inc.
; TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR THE TREATMENT
; FILE REFERENCE: 030639.0032.UT12 (243/131US)
; CURRENT APPLICATION NUMBER: US/09/323,867A
; CURRENT FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 189
; SOFTWARE: PatentIn Ver. 2.1 and Microsoft Word
; SEQ ID NO 171
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: artificial sequence with specific variable residues
; NAME/KEY: MOD RES
; LOCATION: (36)
; OTHER INFORMATION: AMIDATION, Position 36 is Pro-NH2
US-09-323-867A-171

Query Match      62.9%; Score 70.5; DB 4; Length 36;
Best Local Similarity 59.4%; Pred. No. 1.2e-06;
Matches 19; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

Cy      4 GTXXXXXKXEEAVRLXXXXLXGXSXSGA 34
Db      4 GTFTSDASKXEEAVRLFTFLKNGPSSGA 35

RESULT 2
US-09-323-867A-99
; Sequence 99, Application US/09323867A
; Patent No. 6506724
; GENERAL INFORMATION:
; APPLICANT: Amylin Pharmaceuticals, Inc.
; TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR THE TREATMENT
; FILE REFERENCE: 030639.0032.UT12 (243/131US)
; CURRENT APPLICATION NUMBER: US/09/323,867A

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CURRENT FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 189
SOFTWARE: PatentIn Ver. 2.1 and Microsoft Word
SEQ ID NO 99
LENGTH: 37
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: artificial sequence with specific variable residues
NAME/KEY: VARIANT
LOCATION: (31)
OTHER INFORMATION: Xaa is homoproline
NAME/KEY: VARIANT
LOCATION: (36)..(37)
OTHER INFORMATION: Xaa is homoproline
NAME/KEY: MOD RES
LOCATION: (37)
OTHER INFORMATION: AMIDATION, Position 37 is homoproline-NH2
US-09-323-867A-99

Query Match 62.9%; Score 70.5; DB 4; Length 37;
Best Local Similarity 62.5%; Pred. No. 1.2e-06;
Matches 20; Conservative 0; Mismatches 11; Indels 1; Gaps 1;

QY 4 GTXXXXXSKQXEBEAVRLXXXXL-XGXSSGA 34
DB 4 GTFTSDASKQXEBEAVRLFLEWLNKGXSSGA 35

RESULT 3
US-09-323-867A-183
Sequence 183, Application US/09323867A
Patent No. 6506724

GENERAL INFORMATION:
APPLICANT: Amylin Pharmaceuticals, Inc.
TITLE OF INVENTION: USE OF EXTENDING AND AGONISTS THEREOF FOR THE TREATMENT
FILE REFERENCE: 030639.0032.UTL2 (243/131US)
CURRENT APPLICATION NUMBER: US/09/323,867A
CURRENT FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 189
SOFTWARE: PatentIn Ver. 2.1 and Microsoft Word
SEQ ID NO 183
LENGTH: 37
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: artificial sequence with specific variable residues
NAME/KEY: VARIANT
LOCATION: (31)
OTHER INFORMATION: Xaa is N-methylalanine
NAME/KEY: VARIANT
LOCATION: (36)..(37)
OTHER INFORMATION: Xaa is N-methylalanine
NAME/KEY: MOD RES
LOCATION: (37)
OTHER INFORMATION: AMIDATION, Position 37 is N-methylalanine-NH2
US-09-323-867A-183

Query Match 62.9%; Score 70.5; DB 4; Length 37;
Best Local Similarity 62.5%; Pred. No. 1.2e-06;
Matches 20; Conservative 0; Mismatches 11; Indels 1; Gaps 1;

QY 4 GTXXXXXSKQXEBEAVRLXXXXL-XGXSSGA 34
DB 4 GTFTSDASKQXEBEAVRLFLEWLNKGXSSGA 35

RESULT 4
US-09-323-867A-35
Sequence 35, Application US/09323867A
Patent No. 6506724

GENERAL INFORMATION:
APPLICANT: Amylin Pharmaceuticals, Inc.
TITLE OF INVENTION: USE OF EXTENDING AND AGONISTS THEREOF FOR THE TREATMENT
FILE REFERENCE: 030639.0032.UTL2 (243/131US)
CURRENT APPLICATION NUMBER: US/09/323,867A
CURRENT FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 189
SOFTWARE: PatentIn Ver. 2.1 and Microsoft Word
SEQ ID NO 35
LENGTH: 39
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: artificial sequence with specific variable residues
NAME/KEY: VARIANT
LOCATION: (31)
OTHER INFORMATION: Xaa at position 31 is thiopropine
NAME/KEY: VARIANT
LOCATION: (36)..(38)
OTHER INFORMATION: Xaa at positions 36, 37, and 38 is thiopropine
NAME/KEY: MOD RES
LOCATION: (39)
OTHER INFORMATION: AMIDATION, Position 39 is Ser-NH2
US-09-323-867A-35

Query Match 62.9%; Score 70.5; DB 4; Length 39;
Best Local Similarity 62.5%; Pred. No. 1.3e-06;
Matches 20; Conservative 0; Mismatches 11; Indels 1; Gaps 1;

QY 4 GTXXXXXSKQXEBEAVRLXXXXL-XGXSSGA 34
DB 4 GTFTSDASKQXEBEAVRLFLEWLNKGXSSGA 35

RESULT 5
US-09-323-867A-36
Sequence 36, Application US/09323867A
Patent No. 6506724
GENERAL INFORMATION:
APPLICANT: Amylin Pharmaceuticals, Inc.
TITLE OF INVENTION: USE OF EXTENDING AND AGONISTS THEREOF FOR THE TREATMENT
FILE REFERENCE: 030639.0032.UTL2 (243/131US)
CURRENT APPLICATION NUMBER: US/09/323,867A
CURRENT FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 189
SOFTWARE: PatentIn Ver. 2.1 and Microsoft Word
SEQ ID NO 36
LENGTH: 39
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: artificial sequence with specific variable residues
NAME/KEY: VARIANT
LOCATION: (31)
OTHER INFORMATION: Xaa at position 31 is homoproline
NAME/KEY: VARIANT
LOCATION: (36)..(38)
OTHER INFORMATION: Xaa at positions 36, 37, and 38 is homoproline
NAME/KEY: MOD RES
LOCATION: (39)
OTHER INFORMATION: AMIDATION, Position 39 is Ser-NH2
US-09-323-867A-36

Query Match 62.9%; Score 70.5; DB 4; Length 39;
Best Local Similarity 62.5%; Pred. No. 1.3e-06;
Matches 20; Conservative 0; Mismatches 11; Indels 1; Gaps 1;

QY 4 GTXXXXXSKQXEBEAVRLXXXXL-XGXSSGA 34
DB 4 GTFTSDASKQXEBEAVRLFLEWLNKGXSSGA 35

Db 4 GTFTSDLSKQLEBEAVRLFIEFLKNGXSSGA 35

RESULT 6

US-09-323-867A-39
; Sequence 39, Application US/09323867A
; Patent No. 6506724
; GENERAL INFORMATION:
; APPLICANT: Amylin Pharmaceuticals, Inc.
; APPLICANT: Young, Andrew et al.
; TITLE OF INVENTION: USE OF EXTENDING AND AGONISTS THEREOF FOR THE TREATMENT
; FILE REFERENCE: 030639.0032.UTL2 (243/131US)
; CURRENT APPLICATION NUMBER: US/09/323,867A
; CURRENT FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 189
; SOFTWARE: PatentIn Ver. 2.1 and Microsoft Word
; SEQ ID NO 39
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: artificial sequence with specific variable residues
; NAME/KEY: VARIANT
; LOCATION: (31)
; OTHER INFORMATION: Xaa at position 31 is N-methylalanine
; NAME/KEY: VARIANT
; LOCATION: (36)..(38)
; OTHER INFORMATION: Xaa at positions 36, 37, and 38 is N-methylalanine
; NAME/KEY: MOD RES
; LOCATION: (39)
; OTHER INFORMATION: AMIDATION, Position 39 is Ser-NH2
US-09-323-867A-39

Query Match 62.1%; Score 69.5; DB 4; Length 39;
Best Local Similarity 59.4%; Pred. No. 1.8e-06;
Matches 20; Conservative 0; Mismatches 11; Indels 1; Gaps 1;

Qy 4 GTXXXXXSKQEBEAVRLFXXXXL-XGXS SGA 34
Db 4 GTFTSDLSKQLEBEAVRLFIEFLKNGXSSGA 35

RESULT 7

US-09-323-867A-69
; Sequence 69, Application US/09323867A
; Patent No. 6506724
; GENERAL INFORMATION:
; APPLICANT: Amylin Pharmaceuticals, Inc.
; APPLICANT: Young, Andrew et al.
; TITLE OF INVENTION: USE OF EXTENDING AND AGONISTS THEREOF FOR THE TREATMENT
; FILE REFERENCE: 030639.0032.UTL2 (243/131US)
; CURRENT APPLICATION NUMBER: US/09/323,867A
; CURRENT FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 189
; SOFTWARE: PatentIn Ver. 2.1 and Microsoft Word
; SEQ ID NO 69
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: artificial sequence with specific variable residues
; NAME/KEY: MOD RES
; LOCATION: (35)
; OTHER INFORMATION: AMIDATION, Position 35 is Ala-NH2
US-09-323-867A-69

Query Match 62.1%; Score 69.5; DB 4; Length 35;
Best Local Similarity 59.4%; Pred. No. 1.8e-06;
Matches 19; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

Qy 4 GTXXXXXSKQEBEAVRLFXXXXL-XGXS SGA 34

Db 4 GTFTSDLSKQLEBEAVRLFIEFLKNGPSSGA 35

RESULT 8

US-09-323-867A-173
; Sequence 173, Application US/09323867A
; Patent No. 6506724
; GENERAL INFORMATION:
; APPLICANT: Amylin Pharmaceuticals, Inc.
; APPLICANT: Young, Andrew et al.
; TITLE OF INVENTION: USE OF EXTENDING AND AGONISTS THEREOF FOR THE TREATMENT
; FILE REFERENCE: 030639.0032.UTL2 (243/131US)
; CURRENT APPLICATION NUMBER: US/09/323,867A
; CURRENT FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 189
; SOFTWARE: PatentIn Ver. 2.1 and Microsoft Word
; SEQ ID NO 173
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: artificial sequence with specific variable residues
; NAME/KEY: MOD RES
; LOCATION: (35)
; OTHER INFORMATION: AMIDATION, Position 35 is Ala-NH2
US-09-323-867A-173

Query Match 62.1%; Score 69.5; DB 4; Length 35;
Best Local Similarity 59.4%; Pred. No. 1.8e-06;
Matches 19; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

Qy 4 GTXXXXXSKQEBEAVRLFXXXXL-XGXS SGA 34
Db 4 GTFTSDLSKQLEBEAVRLFIEFLKNGPSSGA 35

RESULT 9

US-09-323-867A-67
; Sequence 67, Application US/09323867A
; Patent No. 6506724
; GENERAL INFORMATION:
; APPLICANT: Amylin Pharmaceuticals, Inc.
; APPLICANT: Young, Andrew et al.
; TITLE OF INVENTION: USE OF EXTENDING AND AGONISTS THEREOF FOR THE TREATMENT
; FILE REFERENCE: 030639.0032.UTL2 (243/131US)
; CURRENT APPLICATION NUMBER: US/09/323,867A
; CURRENT FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 189
; SOFTWARE: PatentIn Ver. 2.1 and Microsoft Word
; SEQ ID NO 67
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: artificial sequence with specific variable residues
; NAME/KEY: MOD RES
; LOCATION: (36)
; OTHER INFORMATION: AMIDATION, Position 36 is Pro-NH2
US-09-323-867A-67

Query Match 62.1%; Score 69.5; DB 4; Length 36;
Best Local Similarity 59.4%; Pred. No. 1.8e-06;
Matches 19; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

Qy 4 GTXXXXXSKQEBEAVRLFXXXXL-XGXS SGA 34
Db 4 GTFTSDLSKQLEBEAVRLFIEFLKNGPSSGA 35

RESULT 10

US-09-323-867A-86
Sequence 86, Application US/09323867A
Patent No. 6506724
GENERAL INFORMATION:
APPLICANT: Amylin Pharmaceuticals, Inc.
APPLICANT: Young, Andrew et al.
TITLE OF INVENTION: USE OF EXTENDING AND AGONISTS THEREOF FOR THE TREATMENT
TITLE OF INVENTION: OF GESTATIONAL DIABETES MELLITUS
FILE REFERENCE: 030639.0032.UTL2 (243/131US)
CURRENT APPLICATION NUMBER: US/09/323,867A
CURRENT FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 189
SOFTWARE: PatentIn Ver. 2.1 and Microsoft Word
SEQ ID NO 86
LENGTH: 36
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: artificial sequence with specific variable residues
NAME/KEY: VARIANT
LOCATION: (31)
OTHER INFORMATION: Xaa is homoproline
NAME/KEY: VARIANT
LOCATION: (36)
OTHER INFORMATION: Xaa is homoproline
NAME/KEY: MOD RES
LOCATION: (36)
OTHER INFORMATION: AMIDATION, Position 36 is homoproline-NH2
US-09-323-867A-86

Query Match 62.1%; Score 69.5; DB 4; Length 36;
Best Local Similarity 52.5%; Pred. No. 1.8e-06;
Matches 20; Conservative 0; Mismatches 11; Indels 1; Gaps 1;

QY 4 GTXXXXXSKQXEEBAVRLXXXXL-XGXSXSGA 34
DB 4 GTFTDLSKQMEBAVRLFIEMLNKGXSSGA 35

RESULT 11
US-09-323-867A-170
Sequence 170, Application US/09323867A
Patent No. 6506724
GENERAL INFORMATION:
APPLICANT: Amylin Pharmaceuticals, Inc.
APPLICANT: Young, Andrew et al.
TITLE OF INVENTION: USE OF EXTENDING AND AGONISTS THEREOF FOR THE TREATMENT
TITLE OF INVENTION: OF GESTATIONAL DIABETES MELLITUS
FILE REFERENCE: 030639.0032.UTL2 (243/131US)
CURRENT APPLICATION NUMBER: US/09/323,867A
CURRENT FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 189
SOFTWARE: PatentIn Ver. 2.1 and Microsoft Word
SEQ ID NO 170
LENGTH: 36
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: artificial sequence with specific variable residues
NAME/KEY: MOD RES
LOCATION: (36)
OTHER INFORMATION: AMIDATION, Position 36 is Pro-NH2
US-09-323-867A-170

Query Match 62.1%; Score 69.5; DB 4; Length 36;
Best Local Similarity 59.4%; Pred. No. 1.8e-06;
Matches 19; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

QY 4 GTXXXXXSKQXEEBAVRLXXXXL-XGXSXSGA 34
DB 4 GTFTDLSKQMEBAVRLFIEMLNKGXSSGA 35

RESULT 12
US-09-323-867A-184
Sequence 184, Application US/09323867A
Patent No. 6506724
GENERAL INFORMATION:
APPLICANT: Amylin Pharmaceuticals, Inc.
APPLICANT: Young, Andrew et al.
TITLE OF INVENTION: USE OF EXTENDING AND AGONISTS THEREOF FOR THE TREATMENT
TITLE OF INVENTION: OF GESTATIONAL DIABETES MELLITUS
FILE REFERENCE: 030639.0032.UTL2 (243/131US)
CURRENT APPLICATION NUMBER: US/09/323,867A
CURRENT FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 189
SOFTWARE: PatentIn Ver. 2.1 and Microsoft Word
SEQ ID NO 184
LENGTH: 36
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: artificial sequence with specific variable residues
NAME/KEY: VARIANT
LOCATION: (31)
OTHER INFORMATION: Xaa is homoproline
NAME/KEY: VARIANT
LOCATION: (36)
OTHER INFORMATION: Xaa is homoproline
NAME/KEY: MOD RES
LOCATION: (36)
OTHER INFORMATION: AMIDATION, Position 36 is homoproline-NH2
US-09-323-867A-184

Query Match 62.1%; Score 69.5; DB 4; Length 36;
Best Local Similarity 62.5%; Pred. No. 1.8e-06;
Matches 20; Conservative 0; Mismatches 11; Indels 1; Gaps 1;

QY 4 GTXXXXXSKQXEEBAVRLXXXXL-XGXSXSGA 34
DB 4 GTFTDLSKQMEBAVRLFIEMLNKGXSSGA 35

RESULT 13
US-09-323-867A-65
Sequence 65, Application US/09323867A
Patent No. 6506724
GENERAL INFORMATION:
APPLICANT: Amylin Pharmaceuticals, Inc.
APPLICANT: Young, Andrew et al.
TITLE OF INVENTION: USE OF EXTENDING AND AGONISTS THEREOF FOR THE TREATMENT
TITLE OF INVENTION: OF GESTATIONAL DIABETES MELLITUS
FILE REFERENCE: 030639.0032.UTL2 (243/131US)
CURRENT APPLICATION NUMBER: US/09/323,867A
CURRENT FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 189
SOFTWARE: PatentIn Ver. 2.1 and Microsoft Word
SEQ ID NO 65
LENGTH: 37
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: artificial sequence with specific variable residues
NAME/KEY: MOD RES
LOCATION: (37)
OTHER INFORMATION: AMIDATION, Position 37 is Pro-NH2
US-09-323-867A-65

Query Match 62.1%; Score 69.5; DB 4; Length 37;
Best Local Similarity 59.4%; Pred. No. 1.9e-06;
Matches 19; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

QY 4 GTXXXXXSKQXEEBAVRLXXXXL-XGXSXSGA 34
DB 4 GTFTDLSKQMEBAVRLFIEMLNKGXSSGA 35

```
RESULT 14
US-09-323-867A-83
; Sequence 83, Application US/09323867A
; Patent No. 6506724
; GENERAL INFORMATION:
; APPLICANT: Amylin Pharmaceuticals, Inc.
; TITLE OF INVENTION: USE OF EXTENDING AND AGONISTS THEREOF FOR THE TREATMENT
; FILE REFERENCE: 030639.0032.UTL2 (243/131US)
; CURRENT FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 189
; SOFTWARE: Patentin Ver. 2.1 and Microsoft Word
; SEQ ID NO 83
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: artificial sequence with specific variable residues
; NAME/KEY: VARIANT
; LOCATION: (31)
; OTHER INFORMATION: Xaa is N-methylalanine
; NAME/KEY: MOD_RES
; LOCATION: (37)
; OTHER INFORMATION: AMIDATION, Position 37 is N-methylalanine-NH2
US-09-323-867A-83

Query Match
Best Local Similarity 62.1%; Score 69.5; DB 4; Length 37;
Matches 20; Conservative 0; Mismatches 11; Indels 1; Gaps 1;

Db
4 GTXXXXXKQXEEAVRLXXXXL-XGGSXSGA 34
4 GFTSDLSKQMEBEAVRLFIEWLKNGXSSGA 35

RESULT 15
US-09-323-867A-84
; Sequence 84, Application US/09323867A
; Patent No. 6506724
; GENERAL INFORMATION:
; APPLICANT: Amylin Pharmaceuticals, Inc.
; TITLE OF INVENTION: USE OF EXTENDING AND AGONISTS THEREOF FOR THE TREATMENT
; FILE REFERENCE: 030639.0032.UTL2 (243/131US)
; CURRENT FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 189
; SOFTWARE: Patentin Ver. 2.1 and Microsoft Word
; SEQ ID NO 84
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: artificial sequence with specific variable residues
; NAME/KEY: VARIANT
; LOCATION: (31)
; OTHER INFORMATION: Xaa is N-methylalanine
; NAME/KEY: MOD_RES
; LOCATION: (37)
; OTHER INFORMATION: AMIDATION, Position 37 is N-methylalanine-NH2
US-09-323-867A-84

Query Match
Best Local Similarity 62.1%; Score 69.5; DB 4; Length 37;
Matches 20; Conservative 0; Mismatches 11; Indels 1; Gaps 1;
```

```
Query
Db
4 GTXXXXXKQXEEAVRLXXXXL-XGGSXSGA 34
4 GFTSDLSKQMEBEAVRLFIEWLKNGXSSGA 35

RESULT 16
US-09-323-867A-85
; Sequence 85, Application US/09323867A
; Patent No. 6506724
; GENERAL INFORMATION:
; APPLICANT: Amylin Pharmaceuticals, Inc.
; TITLE OF INVENTION: USE OF EXTENDING AND AGONISTS THEREOF FOR THE TREATMENT
; FILE REFERENCE: 030639.0032.UTL2 (243/131US)
; CURRENT FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 189
; SOFTWARE: Patentin Ver. 2.1 and Microsoft Word
; SEQ ID NO 85
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: artificial sequence with specific variable residues
; NAME/KEY: VARIANT
; LOCATION: (31)
; OTHER INFORMATION: Xaa is homoproline
; NAME/KEY: MOD_RES
; LOCATION: (37)
; OTHER INFORMATION: AMIDATION, Position 37 is homoproline-NH2
US-09-323-867A-85

Query Match
Best Local Similarity 62.1%; Score 69.5; DB 4; Length 37;
Matches 20; Conservative 0; Mismatches 11; Indels 1; Gaps 1;

Query
Db
4 GTXXXXXKQXEEAVRLXXXXL-XGGSXSGA 34
4 GFTSDLSKQMEBEAVRLFIEWLKNGXSSGA 35

RESULT 17
US-09-323-867A-63
; Sequence 63, Application US/09323867A
; Patent No. 6506724
; GENERAL INFORMATION:
; APPLICANT: Amylin Pharmaceuticals, Inc.
; TITLE OF INVENTION: USE OF EXTENDING AND AGONISTS THEREOF FOR THE TREATMENT
; FILE REFERENCE: 030639.0032.UTL2 (243/131US)
; CURRENT FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 189
; SOFTWARE: Patentin Ver. 2.1 and Microsoft Word
; SEQ ID NO 63
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: artificial sequence with specific variable residues
; NAME/KEY: MOD_RES
; LOCATION: (38)
; OTHER INFORMATION: AMIDATION, Position 38 is Pro-NH2
US-09-323-867A-63

Query Match
Best Local Similarity 62.1%; Score 69.5; DB 4; Length 38;
Matches 19; Conservative 0; Mismatches 12; Indels 1; Gaps 1;
```

Qy 4 GTXXXXXSKQXEBAVRLXXXXL-XGXSXSGA 34
Db 4 GTFTSDLSKQLEBAVRLFIETLKNKGXSSGA 35

RESULT 18
US-09-323-867A-81
; Sequence 81, Application US/09323867A
; Patent No. 6506724
; GENERAL INFORMATION:
; APPLICANT: Amylin Pharmaceuticals, Inc.
; APPLICANT: Young, Andrew et al.
; TITLE OF INVENTION: USE OF EXTENDING AND AGONISTS THEREOF FOR THE TREATMENT
; FILE REFERENCE: 030639.0032.UTL2 (243/131US)
; CURRENT APPLICATION NUMBER: US/09/323,867A
; CURRENT FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 189
; SOFTWARE: PatentIn Ver. 2.1 and Microsoft Word
; SEQ ID NO 81
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: artificial sequence with specific variable residues
; NAME/KEY: VARIANT
; LOCATION: (31)
; OTHER INFORMATION: Xaa is thioproline
; NAME/KEY: VARIANT
; LOCATION: (36)..(38)
; OTHER INFORMATION: Xaa is thioproline
; NAME/KEY: MOD RES
; LOCATION: (38)
; OTHER INFORMATION: AMIDATION, Position 38 is thioproline-NH2
US-09-323-867A-81

Query Match 62.1%; Score 69.5; DB 4; Length 38;
Best Local Similarity 62.5%; Pred. No. 1.9e-06;
Matches 20; Conservative 0; Mismatches 11; Indels 1; Gaps 1;
Qy 4 GTXXXXXSKQXEBAVRLXXXXL-XGXSXSGA 34
Db 4 GTFTSDLSKQLEBAVRLFIETLKNKGXSSGA 35

RESULT 19
US-09-323-867A-168
; Sequence 168, Application US/09323867A
; Patent No. 6506724
; GENERAL INFORMATION:
; APPLICANT: Amylin Pharmaceuticals, Inc.
; APPLICANT: Young, Andrew et al.
; TITLE OF INVENTION: USE OF EXTENDING AND AGONISTS THEREOF FOR THE TREATMENT
; FILE REFERENCE: 030639.0032.UTL2 (243/131US)
; CURRENT APPLICATION NUMBER: US/09/323,867A
; CURRENT FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 189
; SOFTWARE: PatentIn Ver. 2.1 and Microsoft Word
; SEQ ID NO 168
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: artificial sequence with specific variable residues
; NAME/KEY: MOD RES
; LOCATION: (38)
; OTHER INFORMATION: AMIDATION, Position 38 is Pro-NH2
US-09-323-867A-168
Query Match 62.1%; Score 69.5; DB 4; Length 38;
Best Local Similarity 59.4%; Pred. No. 1.9e-06;

Matches 19; Conservative 0; Mismatches 12; Indels 1; Gaps 1;
Qy 4 GTXXXXXSKQXEBAVRLXXXXL-XGXSXSGA 34
Db 4 GTFTSDLSKQLEBAVRLFIETLKNKGXSSGA 35

RESULT 20
US-09-323-867A-181
; Sequence 181, Application US/09323867A
; Patent No. 6506724
; GENERAL INFORMATION:
; APPLICANT: Amylin Pharmaceuticals, Inc.
; APPLICANT: Young, Andrew et al.
; TITLE OF INVENTION: USE OF EXTENDING AND AGONISTS THEREOF FOR THE TREATMENT
; FILE REFERENCE: 030639.0032.UTL2 (243/131US)
; CURRENT APPLICATION NUMBER: US/09/323,867A
; CURRENT FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 189
; SOFTWARE: PatentIn Ver. 2.1 and Microsoft Word
; SEQ ID NO 181
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: artificial sequence with specific variable residues
; NAME/KEY: VARIANT
; LOCATION: (31)
; OTHER INFORMATION: Xaa is thioproline
; NAME/KEY: VARIANT
; LOCATION: (36)..(38)
; OTHER INFORMATION: Xaa is thioproline
; NAME/KEY: MOD RES
; LOCATION: (38)
; OTHER INFORMATION: AMIDATION, Position 38 is thioproline-NH2
US-09-323-867A-181

Query Match 62.1%; Score 69.5; DB 4; Length 38;
Best Local Similarity 62.5%; Pred. No. 1.9e-06;
Matches 20; Conservative 0; Mismatches 11; Indels 1; Gaps 1;
Qy 4 GTXXXXXSKQXEBAVRLXXXXL-XGXSXSGA 34
Db 4 GTFTSDLSKQLEBAVRLFIETLKNKGXSSGA 35

RESULT 21
US-09-323-867A-9
; Sequence 9, Application US/09323867A
; Patent No. 6506724
; GENERAL INFORMATION:
; APPLICANT: Amylin Pharmaceuticals, Inc.
; APPLICANT: Young, Andrew et al.
; TITLE OF INVENTION: USE OF EXTENDING AND AGONISTS THEREOF FOR THE TREATMENT
; FILE REFERENCE: 030639.0032.UTL2 (243/131US)
; CURRENT APPLICATION NUMBER: US/09/323,867A
; CURRENT FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 189
; SOFTWARE: PatentIn Ver. 2.1 and Microsoft Word
; SEQ ID NO 9
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: artificial sequence with specific variable residues
; NAME/KEY: MOD RES
; LOCATION: (39)
; OTHER INFORMATION: AMIDATION, Position 39 is Ser-NH2
US-09-323-867A-9
Query Match 62.1%; Score 69.5; DB 4; Length 39;

Best Local Similarity 59.4%; Pred. No. 2e-06;
Matches 19; Conservative 0; Mismatches 12; Indels 1; Gaps 1.

```

QY      4 GTXXXXXSKQEEEAVALXXXXL-XGXSXSGA 34
          ||| ||| ||| ||| ||| ||| ||| |||
DB      4 GTFTSDLSKQLEEAAVRLFIETLKNXGPPSSGA 35

```

RESULT 22
US-09-323-867A-11
; Sequence 11, Application US/09323867A

```

1 GENERAL INFORMATION:
2 APPLICANT: Amylin Pharmaceuticals, Inc.
3 APPLICANT: Young, Andrew et al.
4 TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR THE TREATMENT
5 TITLE OF INVENTION: OF GESTATIONAL DIABETES MELLITUS
6 FILE REFERENCE: 030639.0032.1/TL2 (243/131US)
7 CURRENT APPLICATION NUMBER: US/09/323,867A
8 CURRENT FILING DATE: 1999-06-01
9 NUMBER OF SEQ ID NOS: 189
10 SOFTWARE: PatentIn Ver. 2.1 and Microsoft Word
11 SEQ ID NO 11
12 LENGTH: 39
13 TYPE: PRT
14 ORGANISM: Artificial Sequence
15 FEATURE:
16 OTHER INFORMATION: artificial sequence with specific variable residues
17 NAME/key: MOD RES
18 LOCATION: 139T
19 OTHER INFORMATION: AMIDATION, Position 39 is Ser-NH2
20 US-09-323-867A-11

```

		62.1%	Score 69.5;	DB 4;	length 39;
		Best Local Similarity	59.48;	Pred. No. 2e-06;	
Matches	19;	Conservative	0;	Mismatches	12;
				Indels	1;
				Gaps	1
Oy	4 GTXXXXXSKQEEEAVALXXXXL-XGGAASCA	34			
Dz	4 GTFTSDLSKQWEAEAVRLFIEFLKXGGPSSGA	35			

RESULT 23
US-09-323-867A-21
; Sequence 21, Application US/09323867A

```

1  APPLICANT: Amylin Pharmaceuticals Inc.
2  APPLICANT: Young, Andrew et al.
3  TITLE OF INVENTION: USE OF EXTENDING AND AGONISTS THEREOF FOR THE TREATMENT
4  TITLE OF INVENTION: OF GESTATIONAL DIABETES MELLITUS
5  FILE REFERENCE: 030639.0032.UTTI2 (243/1131US)
6  CURRENT APPLICATION NUMBER: US/09/323,867A
7  CURRENT FILING DATE: 1999-06-01
8  NUMBER OF SEQ ID NOS: 189
9  SOFTWARE: PatentIn Ver. 2.1 and Microsoft Word
10 SEQ ID NO 21
11 LENGTH: 39
12 TYPE: PRT
13 ORGANISM: Artificial Sequence
14 FEATURE:
15 OTHER INFORMATION: artificial sequence with specific variable residues
16 NAME/KEY: MOD RES
17 LOCATION: 139T
18 OTHER INFORMATION: AMIDATION, Position 39 is Ser-NH2
19 NAME/KEY: VARIANT
20 LOCATION: (10)
21 OTHER INFORMATION: Xaa is pentylglycine
22 US-09-323-867A-21

```

Query Match	62.1%;	Score 69.5;	DB 4;	Length 39;
Best Local Similarity	62.5%;	Pred. No. 2e-06;		
Matches	20;	Mismatches	11;	Indels 1;
				Gaps 1;

```
QY      4 GTXXXXXSKQEEBAVRLXXXXL-XGXSXSGA 34
          ||| ||| ||| ||| ||| ||| ||| |||
DB      4 GTFTSDXSKQLEEBAAVRLTIEFLKXNGPSSGA 35
```

RESULT 24
US-09-323-867A-23
: Sequence 23, Application US/09323867A

```

/ APPLICANT: Amylin Pharmaceuticals, Inc.
/ APPLICANT: Young, Andrew et al.
/ TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR THE TREATMENT
/ TITLE OF INVENTION: OF GESTATIONAL DIABETES MELLITUS
/ FILE REFERENCE: 030639.0032.UT/2 (243/131US)
/ CURRENT APPLICATION NUMBER: US/09/323,867A
/ CURRENT FILING DATE: 1999-05-01
/ NUMBER OF SEQ ID NOS: 189
/ SOFTWARE: PatentIn Ver. 2.1 and Microsoft Word
/ SEQ ID NO 23
/ LENGTH: 39
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: artificial sequence with specific variable residues
/ NAME/KEY: MOD RES
/ LOCATION: (39)
/ OTHER INFORMATION: AMIDATION, Position 39 is Ser-NH2
/ NAME/KEY: VARIANT
/ LOCATION: (14)
/ OTHER INFORMATION: Xaa is penlylglycine
/ US-09-323-867A-23

```

Query Match	62.1%	Score 69.5	DB 4	Length 39	.
Best Local Similarity	62.5%	Pred. No. 2e-06			
Matches	20	Conservative	0	Mismatches	11
				Indels	1
				Gaps	1
QY	4	GTXXXXXKQEEBAVRLLXXLL-XGXSSEA	34		
Db	4	GTFTSDLSKQKEEBAVRLEFLNKGSSGA	35		

RESULT 25
US-09-323-867A-26
: Sequence 26, Application US/09323867A

```

1  APPLICANT: Amylin Pharmaceuticals, Inc.
2  APPLICANT: Young, Andrew et al.
3  TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR THE TREATMENT
4  TITLE OF INVENTION: OF GESTATIONAL DIABETES MELLITUS
5  FILE REFERENCE: 030639 0032 URL/2 (243113US)
6  CURRENT APPLICATION NUMBER: US/09/323,867A
7  CURRENT FILING DATE: 1999-06-01
8  NUMBER OF SEQ ID NOS: 189
9  SOFTWARE: PatentIn ver. 2.1 and Microsoft Word
10 SEQ ID NO 26
11 LENGTH: 39
12 TYPE: PRT
13 ORGANISM: Artificial Sequence
14 FEATURE:
15 OTHER INFORMATION: artificial sequence with specific variable residues
16 NAME/KEY: MOD_RES
17 LOCATION: (39)
18 OTHER INFORMATION: AMIDATION, Position 39 is Ser-NH2
19 US-09-323-867A-26

```

Query Match	62.1%	Score 69.5	DB 4	Length 39
Best Local Similarity	59.4%	Pred. No. 2e-06		
Matches 19	Conservative 0	Mismatches 12	Indels 1	Gaps 1
QY	4 GTXXXXXXKXKEEFAVRLXXXXL-XGXSSCA	34		

Db 4 GTFTSDLSKQLEEAVALFVEFLKNGPSSGA 35

RESULT 26
US-09-323-867A-28
Sequence 28, Application US/09323867A
Patent No. 6506724
GENERAL INFORMATION:
APPLICANT: Amylin Pharmaceuticals, Inc.
TITLE OF INVENTION: USE OF EXTENDING AND AGONISTS THEREOF FOR THE TREATMENT
FILE REFERENCE: 030639.0032.UTL2 (243/131US)
CURRENT FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 189
SOFTWARE: PatentIn Ver. 2.1 and Microsoft Word
SEQ ID NO 28
LENGTH: 39
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: artificial sequence with specific variable residues
NAME/KEY: VARIANT
LOCATION: (23)
OTHER INFORMATION: Xaa at position 23 is tertiary-butylglycine
NAME/KEY: MOD.RES
LOCATION: (39)
OTHER INFORMATION: AMIDATION, Position 39 is Ser-NH2
US-09-323-867A-28

Query Match 62.1%; Score 69.5; DB 4; Length 39;
Best Local Similarity 62.5%; Pred. No. 2e-06;
Matches 20; Conservative 0; Mismatches 11; Indels 1; Gaps 1;

Qy 4 GTXXXXXSKQLEEAVALFVEFLKNGPSSGA 34
Db 4 GTFTSDLSKQLEEAVALFVEFLKNGPSSGA 35

RESULT 27
US-09-323-867A-30
Sequence 30, Application US/09323867A
Patent No. 6506724
GENERAL INFORMATION:
APPLICANT: Amylin Pharmaceuticals, Inc.
TITLE OF INVENTION: USE OF EXTENDING AND AGONISTS THEREOF FOR THE TREATMENT
FILE REFERENCE: 030639.0032.UTL2 (243/131US)
CURRENT FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 189
SOFTWARE: PatentIn Ver. 2.1 and Microsoft Word
SEQ ID NO 30
LENGTH: 39
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: artificial sequence with specific variable residues
NAME/KEY: MOD.RES
LOCATION: (39)
OTHER INFORMATION: AMIDATION, position 39 is Ser-NH2
US-09-323-867A-30

Query Match 62.1%; Score 69.5; DB 4; Length 39;
Best Local Similarity 59.4%; Pred. No. 2e-06;
Matches 19; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

Qy 4 GTXXXXXSKQLEEAVALFVEFLKNGPSSGA 34
Db 4 GTFTSDLSKQLEEAVALFVEFLKNGPSSGA 35

RESULT 28
US-09-323-867A-31
Sequence 31, Application US/09323867A
Patent No. 6506724
GENERAL INFORMATION:
APPLICANT: Amylin Pharmaceuticals, Inc.
TITLE OF INVENTION: USE OF EXTENDING AND AGONISTS THEREOF FOR THE TREATMENT
FILE REFERENCE: 030639.0032.UTL2 (243/131US)
CURRENT FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 189
SOFTWARE: PatentIn Ver. 2.1 and Microsoft Word
SEQ ID NO 31
LENGTH: 39
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: artificial sequence with specific variable residues
NAME/KEY: VARIANT
LOCATION: (31)
OTHER INFORMATION: Xaa at position 31 is thioiproline
NAME/KEY: VARIANT
LOCATION: (36)..
OTHER INFORMATION: Xaa at positions 36, 36, and 38 is thioiproline
NAME/KEY: MOD.RES
LOCATION: (39)
OTHER INFORMATION: AMIDATION, Position 39 is Ser-NH2
US-09-323-867A-31

Query Match 62.1%; Score 69.5; DB 4; Length 39;
Best Local Similarity 62.5%; Pred. No. 2e-06;
Matches 20; Conservative 0; Mismatches 11; Indels 1; Gaps 1;

Qy 4 GTXXXXXSKQLEEAVALFVEFLKNGPSSGA 34
Db 4 GTFTSDLSKQLEEAVALFVEFLKNGPSSGA 35

RESULT 29
US-09-323-867A-33
Sequence 33, Application US/09323867A
Patent No. 6506724
GENERAL INFORMATION:
APPLICANT: Amylin Pharmaceuticals, Inc.
TITLE OF INVENTION: USE OF EXTENDING AND AGONISTS THEREOF FOR THE TREATMENT
FILE REFERENCE: 030639.0032.UTL2 (243/131US)
CURRENT FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 189
SOFTWARE: PatentIn Ver. 2.1 and Microsoft Word
SEQ ID NO 33
LENGTH: 39
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: artificial sequence with specific variable residues
NAME/KEY: VARIANT
LOCATION: (31)
OTHER INFORMATION: Xaa at position 31 is homoproline
NAME/KEY: VARIANT
LOCATION: (36)..
OTHER INFORMATION: Xaa at positions 36, 37, and 38 is homoproline
NAME/KEY: MOD.RES
LOCATION: (39)
OTHER INFORMATION: AMIDATION, Position 39 is Ser-NH2
US-09-323-867A-33

Query Match 62.1%; Score 69.5; DB 4; Length 39;
Best Local Similarity 62.5%; Pred. No. 2e-06; 1;
Matches 20; Conservative 0; Mismatches 11; Indels 1; Gaps 1;

QY 4 GTXXXXXSKQEEAVRLXXXXL-XGXSXSGA 34
DB 4 GTFTSDLSKQMEAEAVRLFLEWLKNGXSXSGA 35

RESULT 30

US-09-323-867A-37
; Sequence 37, Application US/09323867A
; Patent No. 6506724
; GENERAL INFORMATION:
; APPLICANT: Amylin Pharmaceuticals, Inc.
; APPLICANT: Young, Andrew et al.
; TITLE OF INVENTION: USE OF EXTENDING AND AGONISTS THEREOF FOR THE TREATMENT
; TITLE OF INVENTION: OF GESTATIONAL DIABETES MELLITUS
; FILE REFERENCE: 030639.0032.UTL2 (243/131US)
; CURRENT APPLICATION NUMBER: US/09/323,867A
; CURRENT FILING DATE: 1999-06-01
; NUMBER OF SEQ. ID NOS: 189
; SOFTWARE: Patentin Ver. 2.1 and Microsoft Word
; SEQ. ID NO 37
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: artificial sequence with specific variable residues
; NAME/KEY: VARIANT
; LOCATION: (31)
; OTHER INFORMATION: Xaa at position 31 is N-methylalanine
; NAME/KEY: VARIANT
; LOCATION: (36)..(38)
; OTHER INFORMATION: Xaa at positions 36, 37, and 38 is N-methylalanine
; NAME/KEY: MOD. RES
; LOCATION: (39)
; OTHER INFORMATION: AMIDATION, position 39 is Ser-NH2
; US-09-323-867A-37

Query Match 62.1%; Score 69.5; DB 4; Length 39;
Best Local Similarity 62.5%; Pred. No. 2e-06; 1;
Matches 20; Conservative 0; Mismatches 11; Indels 1; Gaps 1;

QY 4 GTXXXXXSKQEEAVRLXXXXL-XGXSXSGA 34
DB 4 GTFTSDLSKQMEAEAVRLFLEWLKNGXSXSGA 35

Search completed: December 23, 2003, 10:04:28
Job time: 14.5 secs

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OM protein - protein search, using sw model

Run on: December 23, 2003, 09:59:56 ; Search time 13.5 Seconds
(without alignments)

284,944 Million cell updates/sec

Title: US-09-889-331a-48

Perfect score: 112
Sequence: 1 XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX 40

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283308 seqs, 9616862 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 50 summaries

Database: PIR 76:*

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	68.5	61.2	39	1	HMGH32
2	68.5	61.2	39	1	HMGH32
3	40.5	36.2	458	2	TS1089
4	40.5	36.2	458	2	TS1089
5	39	34.8	189	2	AD2916
6	39	34.8	189	2	AD2916
7	39	34.8	189	2	AD2916
8	39	34.8	189	2	AD2916
9	38.5	34.4	468	2	TS1087
10	38	33.9	208	2	D71137
11	38	33.9	208	2	D71137
12	38	33.9	208	2	D71137
13	38	33.9	208	2	D71137
14	38	33.9	208	2	D71137
15	38	33.9	208	2	D71137
16	38	33.9	208	2	D71137
17	38	33.9	208	2	D71137
18	38	33.9	208	2	D71137
19	38	33.9	208	2	D71137
20	38	33.9	208	2	D71137
21	38	33.9	208	2	D71137
22	38	33.9	208	2	D71137
23	38	33.9	208	2	D71137
24	38	33.9	208	2	D71137
25	38	33.9	208	2	D71137
26	38	33.9	208	2	D71137
27	38	33.9	208	2	D71137
28	38	33.9	208	2	D71137
29	38	33.9	208	2	D71137

30	36	32.1	472	2	A97067	thiamine biosynthe
31	36	32.1	784	2	S26638	SP-1 protein - hu
32	36	32.1	823	2	A36378	probable transcrip
33	36	32.1	1068	1	A44062	genome polypeptide
34	35.5	31.7	382	1	I39848	cell division init
35	35	31.2	129	2	A44828	alkaline phosphata
36	35	31.2	281	2	S2566	actin-binding prot
37	35	31.2	300	2	E71023	probable transcrip
38	35	31.2	300	2	E7110	transcription init
39	35	31.2	338	2	G83508	flagellar motor sw
40	35	31.2	370	2	F66338	protein P2D10.2 (1
41	35	31.2	446	2	A75494	probable Na+/H+ an
42	35	31.2	563	2	A75153	iduronate-2-sulfat
43	35	31.2	803	2	C83561	probable type II s
44	35	31.2	925	2	T02811	DNA excision/repai
45	35	31.2	1029	2	A93363	acetylflavin resista
46	35	31.2	1192	2	S69000	laminin gamma 2 ch
47	35	31.2	1254	2	A54818	myosin-VI [similar
48	35	31.2	1265	2	A59239	unconventional myo
49	34	30.4	85	2	AD0216	conserved hypothet
50	34	30.4	86	2	H95192	hypothetical prote

ALIGNMENTS

RESULT 1

HMGH32

extendin-3 - Mexican beaded lizard

C:Species: Heloderma horridum (Mexican beaded lizard)

C>Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 21-Nov-1997

C:Accession: A23674

R:Eng, J.; Andrews, P.C.; Kleinman, W.A.; Singh, L.; Raufman, J.P.

J. Biol. Chem. 265, 20259-20262, 1990

A:Title: Purification and structure of extendin-3, a new pancreatic secretagogue isolat

A:Reference number: A23674; PMID:91056067; PMID:1700785

A:Accession: A23674

A:Molecule type: protein

A:Residues: 1-39 <ENG>

A:Comment: Extendins are venom components that are thought to bind to receptors for vas

C:Superfamily: Glucagon

C:Keywords: amidated carboxyl end; duplication; secretagogue; venom

F:39/Modified site: amidated carboxyl end (Ser) #status experimental

Query Match 61.2%; Score 68.5; DB 1; Length 39;

Best Local Similarity 59.4%; Pred. No. 3.9e-06; Matches 19; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

QY 4 GTXXXXXKXKXEEAVRLXXXXLXGXSXGA 34

DB 4 GTTSLSKXKXKXEEAVRLFWLKNXGSPSSGA 35

RESULT 2

HMGH32

extendin-4 - Gila monster

C:Species: Heloderma suspectum (Gila monster)

C>Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 21-Nov-1997

C:Accession: A42486

R:Eng, J.; Kleinman, W.A.; Singh, L.; Singh, G.; Raufman, J.P.

J. Biol. Chem. 267, 7402-7405, 1992

A:Title: Isolation and characterization of extendin-4, an extendin-3 analogue, from Helic

A:Reference number: A42486; PMID:92218991; PMID:1331797

A:Accession: A42486

A:Molecule type: protein

A:Residues: 1-39 <ENG>

C:Comment: Extendin-4 does not stimulate amylase secretion by pancreatic acinar cells.

C:Superfamily: Glucagon

C:Keywords: amidated carboxyl end; duplication; venom

F:39/Modified site: amidated carboxyl end (Ser) #status experimental

Query Match 61.2%; Score 68.5; DB 1; Length 39;

```

QY      4 GTXXXXXSKXXEEAVRLXXXL-XGXSSGA 34
          |||         |||         |||         |||
Db      4 GTFSDLSKXMEEEAVRLFLEWLKNXGSPSSGA 35

Best Local Similarity   59.4%;   Pred. No. 3-9e-06;
Matches 19; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

RESULT 3
TS1089
plastid division protein ftsz1 [imported] - moss (Physcomitrella patens)
C:Species: Physcomitrella patens
C>Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 02-Sep-2000
C/Accession: T51089
R:Kuruse, S.; Klessing, J.; Harter, K.; Rensing, S.; Decker, E.; Reski, R.
Submitted to the EMBL Data Library, August 1999
A:Description: Two distinct nuclear-encoded plant ftsZ-genes are highly conserved, both
A:Reference number: 225290
A:Accession: T51089
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-458 <KRU>
A:Cross-references: EMBL:AJ249138; PIDN:CAB54558.1
C:Genetics:
A:Gene: ftsz
A:Introns: 193/3; 293/3; 324/1; 365/3; 396/3; 418/3
C:Superfamily: cell division protein ftsZ
C:Keywords: chloroplast

Query Match           36.2%;   Score 40.5;   DB 2;   Length 458;
Best Local Similarity 33.3%;   Pred. No. 9.7;
Matches 12; Conservative 2; Mismatches 17; Indels 5; Gaps 1;

QY      4 GTXXXXXSKXXEEAVR-----LXXXXLXGXSSGA 34
          |||         |||         |||         |||
Db     169 GCSAAEESKAWVEALRGADWVFVTAGMGCGTSGGA 204

RESULT 4
TS1090
plastid division protein ftsz2 [imported] - moss (Physcomitrella patens)
C:Species: Physcomitrella patens
C>Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 02-Sep-2000
C/Accession: T51090
R:Kuruse, S.; Klessing, J.; Harter, K.; Rensing, S.; Decker, E.; Reski, R.
Submitted to the EMBL Data Library, August 1999
A:Description: Two distinct nuclear-encoded plant ftsZ-genes are highly conserved, both
A:Reference number: 225290
A:Accession: T51090
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-464 <KRU>
A:Cross-references: EMBL:AJ249139; PIDN:CAB76386.1
C:Genetics:
A:Gene: ftsz
A:Introns: 201/3; 301/3; 332/1; 373/3; 404/3; 426/3
C:Superfamily: cell division protein ftsZ
C:Keywords: chloroplast

Query Match           36.2%;   Score 40.5;   DB 2;   Length 464;
Best Local Similarity 33.3%;   Pred. No. 9.9;
Matches 12; Conservative 2; Mismatches 17; Indels 5; Gaps 1;

QY      4 GTXXXXXSKXXEEAVR-----LXXXXLXGXSSGA 34
          |||         |||         |||         |||
Db     177 GCSAAEESKAWVEALRGADWVFVTAGMGCGTSGGA 212

RESULT 5
AD2916
transcription regulator, card family Atuz765 [imported] - Agrobacterium tumefaciens (str. C58)
C:Species: Agrobacterium tumefaciens
C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002

```

```

C:Accession: AD2916
R:Mod, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo,
era, G.; Giller, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McCl
i: Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm
ster, E.W.
A:Title: The genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; WUID:21608550; PMID:11743193
A:Accession: AD2916
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-189 <KIR>
A:Cross-references: GB:AE008686; PIDN:AAU43746.1; PID:g17741280; GSPDB:GN00186
C:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: Atu2765
A:Map position: circular chromosome

Query Match 34.8%; Score 39; DB 2; Length 189;
Best Local Similarity 43.5%; Pred. No. 7.6;
Matches 10; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

OY 11 SKQKEEAVRLXXXXLXGXSSG 33
: |||||
DB 154 NKMSETEAVRLVEYNLAKGPKRG 176

RESULT 6
G97690
Hypothesis: protein AGR_C_5013 [imported] - Agrobacterium tumefaciens (strain C58, C
C:Species: Agrobacterium tumefaciens
C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #ext_change 18-Nov-2002
C:Accession: G97690
R:Goodner, B.; Hinkley, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldm
A: Liu, F.; Wollam, C.; Allinger, M.; Doughy, D.; Scott, C.; Lappas, C.; Markelz, I
Science 294, 2323-2328, 2001
A:Reference number: 294-2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium t
A:Reference number: A97359; WUID:21608551; PMID:11743194
A:Accession: G97690
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-189 <KIR>
A:Cross-references: GB:AE007869; PIDN:AAK8480.1; PID:g15157987; GSPDB:GN00169
C:Genetics:
A:Gene: AGR_C_5013
A:Map position: circular chromosome

Query Match 34.8%; Score 39; DB 2; Length 189;
Best Local Similarity 43.5%; Pred. No. 7.6;
Matches 10; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

OY 11 SKQKEEAVRLXXXXLXGXSSG 33
: |||||
DB 154 NKMSETEAVRLVEYNLAKGPKRG 176

RESULT 7
I40208
cytochrome P450 Bf-1 CYP112 - Bradyrhizobium japonicum
N:Contains: oxidoreductase (EC 1.-.-.-)
C:Species: Bradyrhizobium japonicum
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #ext_change 03-Mar-2000
C:Accession: I40208
R:Tully, R.E.; Keister, D.L.
Appl. Environ. Microbiol. 59, 4135-4142, 1993
A:Title: Cloning and mutagenesis of a cytochrome P-450 locus from Bradyrhizobium japo
A:Reference number: I40207
A:Accession: I40208
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-401 <RES>
A:Cross-references: EMBL:U12678; NID:g529961; PIDN:AAC28889.1; PID:g529962

```

C:Genetics:
 A:Gene: CYP112
 C:Superfamily: Bacillus cytochrome P450 CYP106; cytochrome P450 homology
 C:Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase
 F:234-372/Domain: cytochrome P450 homology <CYP>
 F:350/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 34.8%; Score 39; DB 1; Length 401;
 Best Local Similarity 47.6%; Pred. No. 16;
 Matches 10; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Cy 12 KXSEEAVALXXXXLXGXSSG 32
 Db 221 KASEEAVGLAAGMLVAGHES 241

RESULT 8

unknown protein, 33246-28649 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
 C:Accession: F86457
 R:Thellogis, A.; Ecker, J.R.; Palm, C.J.; Federpiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Com, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
 ansen, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A66141; MUID:21016719; PMID:11130712
 A:Accession: F86457
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-781 <STO>
 A:Cross-references: GB:AE005172; NID:G10645506; PIDN:AA21618.1; GSPDB:GN00141
 C:Genetics:
 A:Map position: 1

Query Match 34.8%; Score 39; DB 2; Length 781;
 Best Local Similarity 50.0%; Pred. No. 32;
 Matches 9; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Cy 17 EAVRLXXXXLXGXSSGA 34
 Db 722 EKVRLASIQLASGDSGA 739

RESULT 9

chloroplast FtsZ-like protein [imported] - common tobacco
 C:Species: Nicotiana tabacum (common tobacco)
 C:Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 02-Sep-2000
 C:Accession: T51087
 R:El-Shami, M.; Alcaraz, J.P.; Leids-Wache, S.; Falcomet, D.
 submitted to the EMBL Data Library, February 2000
 A:Description: A new cDNA encoding FtsZ-like protein from Nicotiana tabacum.
 A:Reference number: Z25288
 A:Accession: T51087
 A:Status: preliminary; translated from GB/EMBL/DBD
 A:Molecule type: mRNA
 A:Residues: 1-468 <ELLS>
 A:Cross-references: EMBL:AJ271750; PIDN:CAB89288.1
 A:Experimental source: variety Bright Yellow 2
 C:Genetics:
 A:Gene: ftsZ
 C:Superfamily: cell division protein ftsZ
 C:Keywords: chloroplast

Query Match 34.4%; Score 38.5; DB 2; Length 468;
 Best Local Similarity 33.3%; Pred. No. 24;

Matches 12; Conservative 2; Mismatches 17; Indels 5; Gaps 1;

Cy 4 GTXXXXXKXSEEAVALXXXXLXGXSSGA 34
 Db 176 GNNANESKQALEEAVYGDWVFTAGMGGTGTGA 211

RESULT 10

probable transcription initiation factor IIB - Pyrococcus horikoshii
 C:Species: Pyrococcus horikoshii
 C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 21-Jul-2000
 C:Accession: D71137
 R:Kawabuchi, Y.; Sawada, M.; Horikawa, H.; Hatakeyama, Y.; Hino, Y.; Yamamoto, S.; Seki,
 M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kishida, N.; Oguchi,
 DNA Res. 5, 55-76, 1998
 A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic
 A:Reference number: A71000; MUID:98344137; PMID:9679194
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-208 <RAW>
 A:Cross-references: GB:AP000003; NID:G3236130; PIDN:BAA2958.1; PID:G3257275
 A:Experimental source: strain OT3
 A>Note: this accession replaces an interim accession for a sequence replaced by GenBank
 C:Genetics:
 A:Gene: PH0864
 C:Superfamily: transcription initiation factor IIB; transcription initiation factor II
 C:Keywords: transcription initiation

Query Match 33.9%; Score 38; DB 2; Length 208;
 Best Local Similarity 36.4%; Pred. No. 13;
 Matches 8; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

Cy 12 KXSEEAVALXXXXLXGXSSG 33
 Db 38 KXVEEAVALXXXXLXGXSSG 59

RESULT 11

probable transport Ecs3230 [imported] - Escherichia coli (strain O157:H7, substrain R1
 C:Species: Escherichia coli
 C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
 C:Accession: F91032
 R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.;
 gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
 DNA Res. 9, 11-22, 2001
 A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and ge
 A:Reference number: A99629; MUID:21156231; PMID:11258796
 A:Accession: F91032
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-310 <NAV>
 A:Cross-references: GB:BA000007; PIDN:BA83653.1; PID:G13362700; GSPDB:GN00154
 A:Experimental source: strain O157:H7, substrain R1MD 0509952
 C:Genetics:
 A:Gene: Ecs3230

Query Match 33.9%; Score 38; DB 2; Length 310;
 Best Local Similarity 34.8%; Pred. No. 19;
 Matches 8; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

Cy 12 KXSEEAVALXXXXLXGXSSGA 34
 Db 50 KXLRDPAVLLMSAIAAGLSMGA 72

RESULT 12

probable transport yfbc [imported] - Escherichia coli (strain O157:H7, substrain EDL93
 C:Species: Escherichia coli
 C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001

0
.
0
C
F
T
T
T
C
C
C

Db 28 EÖTPEEAVEIARAIRGG 4E

Db 28 EQTPEEAVEIARRAIRGG 45

RESULT 17
T06215
glucan endo-1,3-beta-D-glucosidase (EC 3.2.1.39) - barley (fragment)
N/Alternate names: endo-1,3-beta-glucanase
C/Species: Hordeum vulgare (barley)
C/Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 29-Sep-1999
C/Accession: T06215
R/Life: J.C.; Simmons, C.R.; Karre, E.E.; Huang, N.; Rodriguez, R.L.
Eur.J. Biochem. 194, 831-838, 1990
A/Title: The isolation and characterization of a barley 1,3-1,4-beta-glucanase gene.
A/Cross-references: S13830; MUID:91099365; PMID:2148518
A/Accession: T06215
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-328 <L7>
A/Cross-references: EMBL:U06096; NID:92735501; PIDN:AA039322.1; PID:92735502
A/Experimental source: CV: Klages
C/Genetics:
A/Gene: Hv14
C/Superfamily: beta-1,3-glucanase
C/Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 33.0%; Score 37; DB 2; Length 328;
Best Local Similarity 45.0%; Pred. No. 32;
Matches 9; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 15 EEEAVRLXXXXLXGXSXGA 34
| | | | |
Db 181 EPTVQGLVALLGSSSSA 200

RESULT 18
H90168
GRP-binding protein (hGrp) [imported] - Sulfolobus solfataricus
C/Species: Sulfolobus solfataricus
C/Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
C/Accession: H90168
R/Life: O.; Singh, R.K.; Concalonieri, F.; Zivanovic, Y.; Allard, G.; Aways, M.J.; Chan-
aret, R.A.; Ragan, M.A.; Senses, C.W.; Van der Oost, J.
Submitted to GenBank, April 2001
A/Description: Sulfolobus solfataricus complete genome.
A/Reference number: A93139
A/Accession: H90168
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-356 <KTR>
A/Cross-references: GB:AE006641; NID:913813407; PIDN:AA40607.1; GSPDB:GND0155
C/Genetics:
A/Gene: hGrp

Query Match 33.0%; Score 37; DB 2; Length 356;
Best Local Similarity 47.1%; Pred. No. 35;
Matches 8; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 5 TXXXXXSKQXEEAVRL 21
| | | | |
Db 3 TALLVSKFEFEELIAL 19

RESULT 19
A41520
Chromogranin A precursor [validated] - bovine
N/Alternate names: pituitary secretory protein I; secretory protein I
C/Species: Bos primigenius taurus (cattle)
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 18-Aug-2000
C/Accession: A41520; A28033; A24175; A60306; A61114; S15877; S39016; I46008; S38976
R/Life: A.L.; Grimes, M.; Eiden, L.E.
Mol. Endocrinol. 5, 1651-1660, 1991
A/Title: The bovine chromogranin A gene: structural basis for hormone regulation and gen
A/Reference number: A41520; MUID:92140395; PMID:1779968
C/Accession: A41520

A/Status: not compared with conceptual translation
A/Molecule type: DNA
A/Residues: 1-449 <IAC>
A/Cross-references: GB:S79270; NID:9244423; PIDN:AA021297.1; PID:9244424
R/Life: T.G.; Conn, D.V.; Gorr, S.U.; Omsberg, D.L.; Keshden, M.A.; Levine, M.A.
Proc. Natl. Acad. Sci. U.S.A. 84, 5043-5047, 1987
A/Title: Primary structure of bovine pituitary secretory protein I (chromogranin A) de
A/Accession: A28033; MUID:87260925; PMID:3474638
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-111, 'T', 113-190, 'Y', 192-253, 'P', 255-378, 'R', 380-449 <AHN>
A/Cross-references: GB:M16971; NID:9163727; PIDN:AA030765.1; PID:9163728
A/Note: The authors translated the codon CCG for residue 391 as Gln
R/Life: A.L.; Grimes, M.; Eiden, L.E.; Herbert, E.; Grimes, M.
Nature 323, 82-86, 1986
A/Title: Bovine chromogranin A sequence and distribution of its messenger RNA in endoc
A/Reference number: A24175; MUID:86311345; PMID:3018587
A/Accession: A24175
A/Molecule type: mRNA
A/Residues: 1-153, 'PQ', 156-158, 'R', 160-190, 'Y', 192-253, 'P', 255-449 <IAZ>
A/Cross-references: GB:X04298; NID:9217; PIDN:CA027841.1; PID:9218
R/Life: R.; Nakano, I.; Funakoshi, A.; Miyasaka, K.; Ichida, K.; Maki, G.; Arigwin, P.; Chang, D
Regul. Pept. 25, 207-213, 1989
A/Title: Isolation and characterization of bovine pancreaticatin.
A/Reference number: A60306; MUID:89331945; PMID:2756155
A/Accession: A60306
A/Molecule type: Protein
A/Residues: 266-312 <NAK>
R/Life: R.; Barbosa, J.A.; Gill, B.M.; Taklyyuddin, M.A.; O'Connor, D.T.
Endocrinology 128, 174-190, 1991
A/Title: Chromogranin A: posttranslational modifications in secretory granules.
A/Reference number: A61114; MUID:91099142; PMID:1986917
A/Accession: A61114
A/Molecule type: Protein
A/Residues: 19-34, 'X', 36-38, 97-111, 134-139 <BA2>
R/Life: R.; Watson, A.; Joensen, A.C.; Davidson, M.; Young, J.; Lee, C.M.; Moore, S.; Dockray
Biochem. J. 276, 471-479, 1991
A/Title: Heterogeneity of chromogranin A-derived peptides in bovine gut, pancreas and
A/Reference number: S15847; MUID:91264803; PMID:1710890
A/Accession: S15847
A/Molecule type: Protein
A/Residues: 266-310, 'H', 312-318, 'K', 320-331 <WA2>
A/Note: 311-Arg and 319-Glu were also found
R/Life: R.; Watson, A.; Rogers, M.; Dockray, G.J.
Biochem. J. 295, 649-654, 1993
A/Title: Post-translational processing of chromogranin A: differential distribution of
A/Reference number: S39016; MUID:94059013; PMID:8240272
A/Accession: S39016
A/Status: preliminary
A/Molecule type: Protein
A/Residues: 303-331 <WAT>
R/Life: R.; Bendum, U.M.; Baerle, P.A.; Konecki, D.S.; Frank, R.; Powell, J.; Mallet, J.; Hut
EMBO J. 5, 1495-1502, 1986
A/Title: The primary structure of bovine chromogranin A: a representative of a class
A/Reference number: I46008; MUID:86300648; PMID:3755681
A/Accession: I46008
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-135, 'S', 137-190, 'Y', 192-253, 'P', 255-310, 'H', 312-318, 'K', 320-390, 'Q', 392-
A/Cross-references: EMBL:X04012; NID:9197; PIDN:CA027636.1; PID:9198
R/Life: R.; Yoo, S.H.; Ferretti, J.A.
FEBS Lett. 334, 373-377, 1993
A/Title: Nature of the pH-induced conformational changes and exposure of the C-termin
A/Reference number: S38976; MUID:94063061; PMID:8243650
A/Accession: S38976
A/Status: preliminary
A/Molecule type: Protein
A/Residues: 19-26/266-272 <YOO>
C/Comment: Chromogranin A is the major protein of bovine chromogranin granules.
C/Comment: Chromogranin A activity has been demonstrated from proteolytic fragments of
C/Accession: S16/1; 31/3; 63/1; 86/1; 119/1; 266/1; 422/3
C/Superfamily: chromogranin A

C:Keywords: phosphoprotein
 F:1-18/Domain: signal sequence #status predicted <SIG>
 F:19-449/Product: chromatogranin A #status experimental <MAT>
 F:12-161/Product: chromogranin #status predicted <MAT3>
 F:262-312/Product: pancreastatin #status experimental <MAT2>
 F:35-56/Diulfide bonds: #status predicted

Query Match 33.0%; Score 37; DB 1; Length 449;
 Best Local Similarity 42.9%; Pred. No. 44;
 Matches 9; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 11 SKQEEBAVRLXXXXLXGXS 31
 295 SRQEEEMARAPQVLPFGKKS 315

RESULT 20

S71332
 natriuretic peptide clearance receptor - mouse
 N:Alternate names: atrial natriuretic factor clearance receptor
 C:Species: Mus musculus (house mouse)
 C:Date: 23-Jul-1997 #sequence_revision 01-Aug-1997 #text_change 20-Jun-2000
 C:Accession: S71332
 R:Yanaka, N.; Kotera, J.; Tguchi, I.; Sugiura, M.; Kawashima, K.; Omori, K.
 Eur. J. Biochem. 237, 25-34, 1996
 A:Title: Structure of the 5'-flanking regulatory region of the mouse gene encoding the C
 A:Reference number: S71332; MUID:96203905; PMID:8620881
 A:Accession: S71332
 A:Molecule type: mRNA
 A:Status: preliminary
 A:Residues: 1-536 <YAN>
 A:Cross-references: EMBL:D78175; NID:S1514954; PIDN:BA011241.1; PID:G1514955
 C:Superfamily: natriuretic peptide receptor C; natriuretic peptide-binding domain homolo
 C:Keywords: transmembrane protein
 F:126-457/Domain: natriuretic peptide-binding domain homology <NPB>
 F:437-459/Domain: transmembrane #status predicted <TMM>

Query Match 33.0%; Score 37; DB 2; Length 536;
 Best Local Similarity 56.2%; Pred. No. 52;
 Matches 9; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 19 VRLXXXXLXGXS 34
 DB 13 VLARVLGAGSSGA 28

RESULT 21

T13352
 sn-A protein - fruit fly (Drosophila melanogaster)
 C:Species: Drosophila melanogaster
 C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 17-Nov-2000
 C:Accession: T13352
 R:Kelly, L.
 submitted to the EMBL Data Library, May 1998
 A:Reference number: Z17660
 A:Accession: T13352
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-850 <KEP>
 A:Cross-references: EMBL:U54982; NID:G3138877; PID:G3138878; PIDW:AMC1665.1
 C:Genetics:
 A:Cross-references: FlyBase:FBgn0016976

Query Match 33.0%; Score 37; DB 2; Length 850;
 Best Local Similarity 80.0%; Pred. No. 84;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 12 KQEEBAVRL 21
 DB 140 KQEEBAVRL 149

RESULT 22

T13629

probable transcription regulator - Streptomyces coelicolor
 C:Species: Streptomyces coelicolor
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 07-Dec-1999
 C:Accession: T13629
 R:Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A
 submitted to the EMBL Data Library, June 1999
 A:Reference number: 221610
 A:Accession: T13629
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-124 <OLI>
 A:Cross-references: EMBL:AL078610; PIDN:CAB44397.1; GSPDB:GN00070; SCQDB:SC35.30
 A:Experimental source: strain A3(2)
 C:Genetics:
 A:Gene: SCQDB:SC35.30

Query Match 32.6%; Score 36.5; DB 2; Length 124;
 Best Local Similarity 44.0%; Pred. No. 15;
 Matches 11; Conservative 1; Mismatches 10; Indels 3; Gaps 1;

QY 12 KQEEBAVRLXXXXLXGXS 33
 DB 36 RHYEEHVQRVRLVQAFLAAGVSSG 60

RESULT 23

S69070
 hypothetical protein YP084W - yeast (Saccharomyces cerevisiae)
 N:Alternate names: hypothetical protein P9513.5
 C:Species: Saccharomyces cerevisiae
 C:Date: 22-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 19-Apr-2002
 C:Accession: S69070
 R:Couch, J.
 submitted to the EMBL Data Library, March 1996
 A:Description: The sequence of S. cerevisiae cosmid 9513.
 A:Reference number: S69057
 A:Accession: S69070
 A:Molecule type: DNA
 A:Residues: 1-456 <COU>
 A:Cross-references: EMBL:U51033; NID:G1230676; PID:G1230690; GSPDB:GN00016; MIPS:YPR0
 C:Genetics:
 A:Gene: MIPS:YPR084W
 A:Cross-references: SCD:S0006288
 A:Map position: 16R
 C:Superfamily: Saccharomyces cerevisiae hypothetical protein YP084W

Query Match 32.6%; Score 36.5; DB 2; Length 456;
 Best Local Similarity 40.9%; Pred. No. 55;
 Matches 9; Conservative 3; Mismatches 7; Indels 3; Gaps 1;

QY 12 KQEEBAVRLXXXXLXGXS 33
 DB 4 KASEERPRL---AVLGRSTG 22

RESULT 24

E86303
 hypothetical protein Fe11.17 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
 C:Accession: E86303
 R:Theologis, A.; Becker, J.R.; Palm, C.T.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
 Chin, C.W.; Chung, M.K.; Com, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
 ansen, N.E.; Hughes, B.; Huizer, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiz, R.; Marzia
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
 ker, M.; Wu, D.; Yu, G.; Frazer, C.W.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: E86303
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-144 <STD>
 A:Cross-references: GB:AE005172; NID:g9802781; PIDN:AAF9850.1; GSPDB:GN00141
 C:Genetics:
 A:Map position: 1
 Query Match 32.1%; Score 36; DB 2; Length 144;
 Best Local Similarity 34.8%; Pred. No. 21;
 Matches 8; Conservative 6; Mismatches 9; Indels 0; Gaps 0;
 Oy 12 KQEEAVRLXXXXLXGXSSGA 34
 Db 33 KQEEQALKITDHELTGEGTEA 55
 RESULT 25
 C84185
 hypothetical protein Vng0250c [imported] - Halobacterium sp. NRC-1
 C:Species: Halobacterium sp. NRC-1
 C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Dec-2002
 C:Accession: C84185
 R:NG W.V.; Kennedy, S.P.; Mahairas, G.G.; Bergquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Jethava, B.; Keller, K.; Cruz, R.; Danson, M.T.; Hough, D.W.; Maddocks, D.G.; Japid
 Jung, K.H.; Alam, M.; Preitas, T.
 Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
 A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ehardt, H.; Lowe, T.M.; Li
 A:Title: Genome sequence of Halobacterium species NRC-1.
 A:Reference number: A84160; MUID:20504483; PMID:11016950
 A:Accession: C84185
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-249 <STD>
 A:Cross-references: GB:AE004437; NID:g10579889; PIDN:AA618647.1; GSPDB:GN00138
 C:Genetics:
 A:Gene: VNG0250C
 C:Superfamily: uncharacterized conserved protein
 Query Match 32.1%; Score 36; DB 2; Length 249;
 Best Local Similarity 42.1%; Pred. No. 37;
 Matches 8; Conservative 2; Mismatches 9; Indels 0; Gaps 0;
 Oy 16 EEAVALXXXXLXGXSSGA 34
 Db 231 EAALPAERIRGMSGA 249
 RESULT 26
 S53321
 cytochrome B561 - human
 C:Species: Homo sapiens (man)
 C:Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 07-May-1999
 C:Accession: S53321
 R:Stravastava, M.; Gibson, K.R.; Pollard, H.B.; Fleming, P.J.
 Biochem. J. 303, 915-921, 1994
 A:Title: Human cytochrome b561: a revised hypothesis for conformation in membranes whi
 A:Reference number: S53321; MUID:95071309; PMID:7980462
 A:Accession: S53321
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-251 <STR>
 A:Cross-references: EMBL:U06715
 C:Genetics:
 A:Gene: GDB:CYB561
 A:Cross-references: GDB:228138
 A:Map position: 17q11-17qter
 Query Match 32.1%; Score 36; DB 2; Length 251;
 Best Local Similarity 36.4%; Pred. No. 37;
 Matches 8; Conservative 4; Mismatches 10; Indels 0; Gaps 0;
 Oy 13 QXEEAVRLXXXXLXGXSSGA 34

Db 229 QAEQALSMDFKTLRGCDSPGS 250

RESULT 27

UC6198
alpha-tropomyosin C-2 - axolotl
C:Species: *Amylostoma mexicanum* (axolotl)
C:Date: 11-Apr-1997 #sequence_rev1997 #text_change 13-Aug-1999
C:Accession: J06198
R:Linque, E.A.; Spinner, B.J.; Dube, S.; Dube, D.K.; Lemanski, L.F.
Gene 185, 175-180, 1997
A:Title: Differential expression of a novel isoform of alpha-tropomyosin in cardiac and skeletal muscle of the axolotl
A:Reference number: J06198; MUID:97208870; PMID:9055812
A:Contents: Heart
A:Accession: J06198
A:Residues: 1-284 <LNU>
A:Molecule type: mRNA
A:Cross-references: GB:J33449; NID:q1871355; PIDN:AA060091.1; PID:q1871356
C:Comment: This protein is a actin-binding protein.
C:Genetic8:
A:Gene: *ATMC-2*
C:Superfamily: tropomyosin
C:Keywords: actin binding

Query Match 32.1%; Score 36; DB 2; Length 284;
Best Local Similarity 72.7%; Pred. No. 42;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Cy 11 SKQEEFAYRL 21
Db 36 SKQEEFAYRL 46

RESULT 28

D75311
conserved hypothetical protein - *Deinococcus radiodurans* (strain R1)
C:Species: *Deinococcus radiodurans*
C:Date: 03-Dec-1999 #sequence_rev1999 #text_change 17-Mar-2000
C:Accession: D75311
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; M. Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Uitterback, T.; Zalewski, C.; S. Smith, H.O.; Venner, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium *Deinococcus radiodurans* R1.
A:Reference number: A75250; MUID:20016896; PMID:10567266
A:Accession: D75311
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-344 <WHI>
A:Cross-references: GB:AE002048; GB:AE000513; NID:g6459929; PIDN:AAF11687.1; PID:g6459929
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR2143
A:Map position: 1
C:Superfamily: erythrocyte band 7 integral membrane protein

Query Match 32.1%; Score 36; DB 2; Length 344;
Best Local Similarity 41.2%; Pred. No. 52;
Matches 7; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Cy 13 QXEEFAYRLXXXXLXGG 29
Db 232 QAEFAYRVVSGAIAAG 248

RESULT 29

A75054
polydiphenyl cofactor biosynthesis protein (moa-1) *PAH1436 - Pyrococcus abyssi* (strain C)
C:Species: *Pyrococcus abyssi*
C:Date: 20-Aug-1999 #sequence_rev1999 #text_change 20-Jun-2000
C:Accession: A75054
C:anonymous, Genoscope

submitted to the EMBL Data Library, July 1999

A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru

A:Reference number: A75001

A:Accession: A75054

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-402 <KAM>

A:Cross-references: GB:AU248287, GB:AU096836, NID:G5458657, PIDN:CAB50326.1, PID:G545883

A:Experimental source: strain Orsay

C:Genetics:

A:Gene: PAB1436

C:Superfamily: molybdenum cofactor biosynthesis protein moeA-2

Query Match 32.1%; Score 36; DB 2; Length 402;

Best Local Similarity 36.4%; Pred. No. 60;

Matches 8; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 12 KQEEAVRLXXXLXGXSQ 33

DB 237 KELIEGVVADIVISGASG 258

RESULT 30

A97067

Chiamine biosynthesis enzyme ThH [imported] - Clostridium acetobutylicum

C:Species: Clostridium acetobutylicum

C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001

C:Accession: A97067

R:Noilling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,

.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.

J. Bacteriol. 183, 4823-4838, 2001

A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo

A:Reference number: A96900; MUID:21359325; PMID:21359325

A:Accession: A97067

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-472 <KUR>

A:Cross-references: GB:AE001437, PIDN:AAK79324.1, PID:G15024290, GSPDB:GN00168

A:Experimental source: Clostridium acetobutylicum ATCC824

C:Genetics:

A:Gene: CAC1356

Query Match 32.1%; Score 36; DB 2; Length 472;

Best Local Similarity 31.8%; Pred. No. 71;

Matches 7; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 11 SKQEEAVRLXXXLXGXSQ 32

DB 322 SKTRREYELGISQSGSSST 343

Search completed: December 23, 2003, 10:02:40
Job time : 15.5 secs

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OM protein - protein search, using sw model

Run on: December 23, 2003, 09:59:56 / Search time 10 Seconds

(without alignments)
188.107 Million cell updates/sec

Title: US-09-889-331A-48

Perfect score: 112
Sequence: 1 XXXXTXXXXXKXQXEEAVRLXXXXLXGXSXGAXXXXX 40

Scoring table: BLOSUM62
Gap 10.0, Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database: SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	68.5	61.2	39	1	EXE3_HELHO
2	68.5	61.2	87	1	EXE3_HELHO
3	39	34.8	401	1	CEAP_BRAVA
4	38	33.9	310	1	YFDC_ECOLI
5	38	33.9	512	1	Y4WA_RHISN
6	37	33.0	248	1	PCRB_METTH
7	37	33.0	251	1	CS61_HUMAN
8	37	33.0	449	1	CMGA_BOVIN
9	37	33.0	536	1	ANPC_MOUSE
10	36	32.1	344	1	VU79_HAYEU
11	36	32.1	784	1	SP4_HUMAN
12	36	32.1	823	1	NUC1_NUCR
13	36	32.1	1049	1	CARB_SULTO
14	36	32.1	3068	1	POLG_PEMVC
15	35.5	31.7	382	1	FTSZ_BACSU
16	35	31.2	300	1	TF2B_PYRAB
17	35	31.2	300	1	TF2B_PYRAB
18	35	31.2	300	1	FLIG_PSDAE
19	35	31.2	382	1	LMXA_HUMAN
20	35	31.2	407	1	ASSY_SHEON
21	35	31.2	563	1	IDS_MOUSE
22	35	31.2	735	1	MKLN_HUMAN
23	35	31.2	735	1	MKLN_MOUSE
24	35	31.2	735	1	MKLN_MOUSE
25	35	31.2	1191	1	LMG2_MOUSE
26	35	31.2	1262	1	MYO6_HUMAN
27	35	31.2	1265	1	MYO6_MOUSE
28	34	30.4	85	1	YH74_YERPE
29	34	30.4	248	1	TPIS_MACMU
30	34	30.4	338	1	ARGC_LEPIN
31	34	30.4	400	1	CEXP_RHISN
32	34	30.4	485	1	VG14_BPMMD
33	34	30.4	535	1	ANPC_RAT

34	34	30.4	620	1	Y886_METJA	Q58296 methanococ
35	34	30.4	665	1	ENV_MLYMO	P03385 moloney mur
36	34	30.4	723	1	Y552_HUMAN	O60299 homo sapien
37	34	30.4	723	1	Y552_HUMAN	O24143 drosophila
38	34	30.4	862	1	CNRC_CHICK	P52731 gallus gall
39	34	30.4	982	1	L110_CAREL	O17583 caenorhabdi
40	34	30.4	1097	1	KRID_RAT	O35787 rattus norv
41	34	30.4	1103	1	KRIC_HUMAN	O48966 homo sapien
42	34	30.4	1905	1	TAGB_DICDI	P54683 dicystosteli
43	33	29.5	135	1	RK16_GRATE	P16633 graciilaria
44	33	29.5	289	1	TXNL_HUMAN	O43396 homo sapien
45	33	29.5	302	1	SYGA_MIGBR	O68124 wiglesworth
46	33	29.5	316	1	Y885_MYCPN	P75300 mycoplasma
47	33	29.5	337	1	LEPL_ECOLI	P32099 escherichia
48	33	29.5	378	1	RECA_FUSIN	O81fy0 fusobacteri
49	33	29.5	466	1	VP19_HSVZG	P22486 herpes simp
50	33	29.5	466	1	VP19_HSVZH	P89461 herpes simp

ALIGNMENTS

RESULT 1

EXE3_HELHO STANDARD; PRT; 39 AA.

AC P20394:

DT 01-FEB-1991 (Rel. 17, Last sequence update)

DT 01-FEB-1991 (Rel. 17, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Exendin-3.

OS Heloderma horridum horridum (Mexican beaded lizard).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidodonta; Squamata; Scleroglossa; Anguilliformes; Helodermatidae;

OC Heloderma.

OK NCBI_TaxID=8552;

RN (1)

RP SEQUENCE.

RC TISSUE=Venom;

RA Eng J., Andrew P.C., Kleinman W.A., Singh L., Rautman J.P.;

RT "Purification and structure of exendin-3, a new pancreatic

RL J. Biol. Chem. 265:20259-20262 (1990).

CC -1- FUNCTION: Has a VIP/secretin-like biological activity. Interacts

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.

CC -1- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.

DR PIR, A23674; HG332.

DR HSSP, P01275; IER0.

DR InterPro, IPR000532; Glucagon.

DR Pfam, PF00123; hormone2.1.

DR SMART, SM00070; GLUCA.1.

DR PROSITE, PS00260; GLUCAGON.1.

KW Glucagon family; Toxin; Amidation.

FT MOD_RES 39 AA; 4204 MW; A44251D9A4IDB9 CRC64;

SQ SEQUENCE 39 AA; 4204 MW; A44251D9A4IDB9 CRC64;

Query Match 61.2%; Score 68.5; DB 1; Length 39;

Best Local Similarity 59.4%; Pred. No. 1.3e-06;

Matches 19; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

QY 4 GTXXXXXKXQXEEAVRLXXXXLXGXSXGSA 34

Db 4 GTTSDLSKXQXEEAVRLFIETWLNKXGSSGA 35

RESULT 2

EXE3_HELHO STANDARD; PRT; 87 AA.

ID P26349:

DT 01-MAY-1992 (Rel. 22, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Exendin-4 precursor. (Gila monster)

OS Heloderma suspectum (Chilomeniscus)

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Lepidodermata; Squamata; Scleroglossa; Anguilliformes; Helodermatidae;

OC Heloderma.

OX NCBI_TaxID=8554;

RN [1]

RP SEQUENCE FROM N.A.

RC MEDLINE=9172477; PubMed=9020121;

RA Chen Y.E., Drucker D.J.;

RT "Tissue-specific expression of unique mRNAs that encode proglucagon-derived peptides or exendin 4 in the lizard."

RL J. Biol. Chem. 272:4108-4115(1997).

RN [2]

RP SEQUENCE OF 48-86.

RC TISSUE=Venom;

RA Eng J., Kleinman W.A., Singh L., Singh G., Raufman J.-P.;

RT "Isolation and characterization of exendin-4, an exendin-3 analogue, from Heloderma suspectum venom. Further evidence for an exendin receptor on dispersed acini from guinea pig pancreas."

RL J. Biol. Chem. 267:7402-7405(1992).

CC -1- FUNCTION: Has a VIP/secrecin-like biological activity. Interacts with the exendin receptor.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.

CC -1- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.

CC -----

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CC -----

DR EMBL: U77613; AAB51130.1; -

DR PIR: A42486; HMGH4G.

DR PDB: 1URJ; 21-NOV-01.

DR InterPro: IPR000532; Glucagon.

DR Pfam: PF00123; hormone2.1.

DR SMART: SM00070; GLUCA.1.

DR PROSITE: PS00260; GLUCAGON.1.

DR Glucagon family; Toxin; Amidation; Signal; 3D-structure.

KM SIGNAL 1 23 POTENTIAL.

FT PROPEP 24 47

FT PEPTIDE 48 86 EXENDIN-4.

FT MOD RES 86 86 AMIDATION (G-87 PROVIDE AMIDE GROUP).

SO SEQUENCE 87 AA; 9479 MW; 656BA6E3D87454A2 CRC64;

QY Query Match 61.2%; Score 68.5; DB 1; Length 87;

DB Best Local Similarity 59.4%; Pred. No. 3e-06; Mismatches 12; Indels 1; Gaps 1;

Matches 19; Conservative 0;

4 GTXXXXXSKXEEAVRLXXXXL-XGXSSGA 34

51 GFTSDLSKOMEBAVRLFIWLKNGCPSSGA 82

RESULT 3

CXP BRAJA STANDARD; PRT; 401 AA.

AC Q59203;

DT 01-NOV-1997 (Rel. 35, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Cytochrome P450 Br-1 (EC 1.14.14.-) (Cytochrome P450 112).

GN CYP112 OR BR2144

OS Bradyrhizobium japonicum.

OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;

OC Bradyrhizobiaceae; Bradyrhizobium.

OX NCBI_TaxID=375;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=USDA 110;

RA Tully R.E., Keister D.L.;

RT "Cloning and mutagenesis of a cytochrome P-450 locus from Bradyrhizobium japonicum that is expressed anaerobically and symbiotically."

RL Appl. Environ. Microbiol. 59:4136-4142(1993).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=USDA 110;

RA MEDLINE=9832110; PubMed=9655913;

RA Tully R.E., van Berkum P., Lovins K.W., Keister D.L.;

RT "Identification and sequencing of a cytochrome P450 gene cluster from Bradyrhizobium japonicum."

RL Biochim. Biophys. Acta 1398:243-255(1998).

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=USDA 110;

RA MEDLINE=22484998; PubMed=12597275;

RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.;

RA Sasamoto S., Watanabe A., Ideawa K., Irituchi M., Kawashima K.;

RA Kohara M., Matsunojo M., Shimpo S., Teurloka H., Wada T., Yamada M.;

RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium Bradyrhizobium japonicum USDA110."

RL DNA Res. 9:189-197(2002).

CC -1- FUNCTION: CYTOCHROMES P450 ARE A GROUP OF HEME-THIOLATE MONOOXYGENASES. THEY OXIDIZE A VARIETY OF STRUCTURALLY UNRELATED COMPOUNDS, INCLUDING STEROIDS, FATTY ACIDS, AND XENOBIOTICS.

CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.

CC -----

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CC -----

DR EMBL: U12678; AAC28889.1; -

DR EMBL: AP005942; BAC47409.1; -

DR PIR: I40208; 140208.

DR HSP: O00441; 10XA.

DR InterPro: IPR001128; Cytochrome_P450.

DR Pfam: PF00067; P450.1.

DR PRINTS: PRO0385; P450.

DR PROSITE: PS00086; CYTOCHROME_P450.1.

KM Oxidoreductase; Monooxygenase; Electron transport; Heme;

KM Complete proteome.

FT METAL 350

FT CONFLICT 251 251 L -> H (IN REF. 1 AND 2).

FT CONFLICT 275 275 E -> Q (IN REF. 1 AND 2).

SO SEQUENCE 401 AA; 44473 MW; 41DF690D11FD045A CRC64;

QY Query Match 34.8%; Score 39; DB 1; Length 401;

DB Best Local Similarity 47.6%; Pred. No. 6.8; Mismatches 11; Indels 0; Gaps 0;

Matches 10; Conservative 0;

12 KXEEAVRLXXXXLXGXSS 32

221 KASEEAVGLAAGMLVAGHS 241

RESULT 4

YFDC ECOLI STANDARD; PRT; 310 AA.

AC P37327;

DT 01-OCT-1994 (Rel. 30, Created)

DT 01-OCT-1994 (Rel. 30, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Hypothetical protein yfbc.

GN YFDC OR B2347.

OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RA Baumann S.;
 RL Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12 / MG1655;
 RX MEDLINE=97426617; PubMed=9278503;
 RA Blattner F.R., Plunkett G. II, Bloch C.A., Bernal N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RL "The complete genome sequence of Escherichia coli K-12.";
 Science 277:1453-1474(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE=97349980; PubMed=9205837;
 RA Yanamoto Y., Alta H., Baba T., Hayashi K., Inada T., Isono K.,
 RA Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsunashi N.,
 RA Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nishimoto H.,
 RA Oshima T., Oyama S., Saito N., Sempel G., Satoh Y., Sivasubraman S.,
 RA Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada C.,
 RA Yamagata S., Horuchi T.;
 RL "Construction of a contiguous 874-kb sequence of the Escherichia coli
 RT K-12 genome corresponding to 50,068.8 min on the linkage map and
 RT analysis of its sequence features.";
 DNA Res. 4:91-113(1997).
 RN [4]
 RP IDENTIFICATION.
 RA Rudd K.E.;
 RL Unpublished observations (AUG-1994).
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 CC -----
 DR EMBL; AE000323; AAC75407.1; -
 DR EMBL; D90865; BA16207.1; -
 DR EMBL; U11296; -; NOT_ANNOTATED_CDS.
 DR PIR; A65008; A65008.
 DR EcGene; EG12420; Yfcd.
 KW Hypothetical protein; Complete proteome.
 SO SEQUENCE 310 AA; 34503 MW; 96D34F450B209ED3 CRC64;
 QY Query Match 33.9%; Score 38; DB 1; Length 310;
 Best Local Similarity 34.8%; Pred. No. 8;
 Matches 8; Conservative 4; Mismatches 11; Indels 0; Gaps 0;
 Db 12 KQXEEAVRLXXXXLXGXSSGA 34
 50 KELEKDMALMWSAIAAGLSMGA 72
 RESULT 5
 Y4WA RHISN STANDARD; PRT; 512 AA.
 AC P55679;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Hypothetical zinc protease Y4WA (EC 3.4.99.-).
 GN Y4WA.
 OS Rhizobium sp. (strain NGR234).

OG Plasmid sym PNGR234a.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
 OX NCBI_TaxID=394;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=97305956; PubMed=9163424;
 RA Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,
 RA Perret X.;
 RL "Molecular basis of symbiosis between Rhizobium and legumes.";
 Nature 387:394-401(1997).
 CC -1- CORRELATOR: REQUIRES DIVALENT CATIONS FOR ACTIVITY. BINDS ZINC (BY
 CC SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M16.
 CC -1- SIMILARITY: TO Y4WB.
 CC -----
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 CC -----
 DR EMBL; AE000103; AAB91908.1; -
 DR MEROPS; M16 UPB; -
 DR InterPro; IPR001431; Peptidase_M16.
 DR Pfam; PF00675; Peptidase_M16; 1.
 DR Pfam; PF05193; Peptidase_M16_C1.
 DR PROSITE; PS00143; INSULINASE; 1.
 KW Hypothetical protein; Hydrolase; Metalloprotease; Zinc;
 KM Transmembrane; Plasmid.
 FT TRANSMEM 57 77
 FT METAL 131 131 POTENTIAL.
 FT ACT_SITE 134 134 ZINC (BY SIMILARITY).
 FT METAL 135 135 ZINC (BY SIMILARITY).
 FT METAL 211 211 ZINC (BY SIMILARITY).
 SQ SEQUENCE 512 AA; 56886 MW; 7BD0C60C1F08BD85 CRC64;
 QY Query Match 33.9%; Score 38; DB 1; Length 512;
 Best Local Similarity 32.1%; Pred. No. 14;
 Matches 9; Conservative 4; Mismatches 15; Indels 0; Gaps 0;
 Db 5 TXXXXXSKQXEEAVRLXXXXLXGXSS 32
 335 TSYGAEQGAALDIILSEILGGGTRS 362
 RESULT 6
 PCRB METH STANDARD; PRT; 248 AA.
 ID PCRB METH
 AC Q26652;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE PezB protein homolog.
 GN PezB OR MTH552.
 OS Methanobacterium thermoautotrophicum.
 OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
 OC Methanobacteriaceae; Methanothermobacter.
 OX NCBI_TaxID=187420;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Deleia H;
 RX MEDLINE=98037514; PubMed=93711463;
 RA Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,
 RA Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
 RA Harrison D., Hoang L., Keagle P., Lum W., Pothier B., Qiu D.,
 RA Spadefora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
 RA Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
 RA McDougall S., Shiner G., Goyal A., Pietrovski S., Church G.M.,
 RA Daniels C.T., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
 RL "Complete genome sequence of Methanobacterium thermoautotrophicum

RT deltaH: functional analysis and comparative genomics."
 RL J. Bacteriol. 179:7135-7155(1997).
 CC -1- SIMILARITY: Belongs to the pcrB family.
 CC -----
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 CC -----
 DR EMBL: A6006838; AAB85058.1; -
 DR PIR: A69173; A69173.1
 DR HAMAP: MF_00112; 1
 DR InterPro: IPR003009; F0M1_enzyme.
 DR InterPro: IPR002911; PcrB.
 DR Pfam: PF01884; PcrB.1
 DR TIGRFAMs: TIGR00265; TIGR00265.1
 KM Complete proteome.
 SQ SEQUENCE 248 AA; 26525 MW; F59DAE240731E662 CRC64;
 Query Match 33.0%; Score 37; DB 1; Length 248;
 Best Local Similarity 36.4%; Pred. No. 9.9;
 Matches 7; Conservative 3; Mismatches 8; Indels 0; Gaps 0;
 Oy 12 KQEEAVRLXXXXXGSG 29
 Db 28 EQTEAEVETARAIRG 45
 RESULT 7
 ID C561 HUMAN STANDARD; PRT; 251 AA.
 AC P49447; Q9B0U5; Q9BWR9;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Cytochrome b561 (Cytochrome b-561).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Peritoneal blood.
 RX MEDLINE=96032691; PubMed=7559396;
 RA Srivastava M.;
 RT "Genomic structure and expression of the human gene encoding
 RT cytochrome b561, an integral protein of the chromaffin granule
 RT membrane".
 RL J. Biol. Chem. 270:22714-22720(1995).
 RN (2)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain, and Lung;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Klausner R.D., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Hopfner R.F., Zeeberg B., Buechow K.H., Schaefer C.F., Bhat N.K.,
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stabileton M., Soares W.B., Bonaldi M.F., Cavaletto T.L., Schetz T.E.,
 RA Brownstein M.J., Ussid T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loguettano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gamaralle P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Huliy S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kerteman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman U.W., Green B.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,
 RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,

RA Schercher A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences".
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN (3)
 RP SEQUENCE OF 6-251 FROM N.A.
 RC TISSUE=Caudate;
 RX MEDLINE=95071309; PubMed=7980462;
 RA Srivastava M., Gibson K.R., Pollard H.B., Fleming P.J.,
 RT "Human cytochrome b561: a revised hypothesis for conformation in
 RT membranes which reconciles sequence and functional information".
 RL Biochem. J. 303:915-921(1994)
 CC -1- FUNCTION: SECRETORY VESICLE-SPECIFIC ELECTRON TRANSPORT PROTEIN.
 CC -1- COPACITOR: BINDS TWO HEME GROUPS NON-COVALENTLY (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE EUKARYOTIC B561 FAMILY.
 CC -----
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 CC -----
 DR EMBL: U29462; AAC50212.1; -
 DR EMBL: U29460; AAC50212.1; JOINED.
 DR EMBL: U29461; AAC50212.1; JOINED.
 DR EMBL: U29464; AAC50212.1; JOINED.
 DR EMBL: U29469; AAC50212.1; JOINED.
 DR EMBL: BC000021; AAH00021.1; -
 DR EMBL: BC002976; AAH02976.1; -
 DR EMBL: U06715; AAB50952.1; -
 DR PIR: S53321; S53321.
 DR Genew: HGNC:2571; CYP561.
 DR MIM: 600019; -
 DR GO: GO:0005887; C: integral to plasma membrane; TAS.
 DR GO: GO:0005804; C: secretory vesicle membrane; TAS.
 DR GO: GO:0005803; C: secretory vesicle; TAS.
 DR GO: GO:0004128; F: cytochrome b5 reductase activity; TAS.
 DR GO: GO:0006091; P: energy pathways; TAS.
 DR InterPro: IPR004877; Cyt_b561.
 DR InterPro: IPR006593; Cyt_b561_Fer-ox.
 DR Pfam: PF03188; Cytochrome B561; 1.
 DR SMART: SMO0665; B561; 1.
 DR KM Electron transport; Transmembrane; Heme.
 FT DOMAIN 1 15 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 16 38 POTENTIAL.
 FT TRANSMEM 33 75 POTENTIAL.
 FT TRANSMEM 85 107 POTENTIAL.
 FT TRANSMEM 123 145 POTENTIAL.
 FT TRANSMEM 163 185 POTENTIAL.
 FT TRANSMEM 197 219 POTENTIAL.
 FT DOMAIN 220 251 POTENTIAL.
 FT METAL 53 53 IRON (HEME AXIAL LIGAND) (POTENTIAL).
 FT METAL 87 87 IRON (HEME AXIAL LIGAND) (POTENTIAL).
 FT METAL 91 91 IRON (HEME AXIAL LIGAND) (POTENTIAL).
 FT METAL 109 109 IRON (HEME AXIAL LIGAND) (POTENTIAL).
 FT METAL 121 121 IRON (HEME AXIAL LIGAND) (POTENTIAL).
 FT METAL 160 160 IRON (HEME AXIAL LIGAND) (POTENTIAL).
 FT CONFLICT 6 6 A -> S (IN REF. 2; AAH02976).
 FT CONFLICT 171 171 S -> P (IN REF. 1 AND 3).
 FT CONFLICT 243 244 TE -> RO (IN REF. 1 AND 3).
 SQ SEQUENCE 251 AA; 27559 MW; 8BE53AE4D2569877 CRC64;
 Query Match 33.0%; Score 37; DB 1; Length 251;
 Best Local Similarity 36.4%; Pred. No. 10;
 Matches 8; Conservative 4; Mismatches 10; Indels 0; Gaps 0;
 Oy 13 QXEEAVRLXXXXXGSGSGA 34
 Db 229 QAEQALSMDFKLTLEDSPGS 250

RESULT 8
CMGA BOVIN STANDARD; PRT; 449 AA.
ID CMGA BOVIN STANDARD; PRT; 449 AA.
AC P05059; P79392;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Chromogranin A precursor (CGA) (Pituitary secretory protein I) (SP-1)
DE [contains: Vasoactive-1; Chromostatin; Chromacin; Pancreastatin; WE-
14; Catestatin].
GN CHGA
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI Taxid:9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92140395; PubMed=1779968;
RA Taccangelo A.L., Grimes M., Eiden L.E.;
RT "The bovine chromogranin A gene: structural basis for hormone
RT regulation and generation of biologically active peptides.";
RL Mol. Endocrinol. 5:1651-1660(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=86300648; PubMed=3755681;
RA Benedum U.M., Baueverle P.A., Konecki D.S., Frank R., Powell J.,
RA Mallet U., Hutterer M.B.;
RT "The primary structure of bovine chromogranin A: a representative of
RT a class of acidic secretory proteins common to a variety of
RT peptidergic cells.";
RL EMBO J. 5:1495-1502(1986).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=86311345; PubMed=3016587;
RA Taccangelo A.L., Alfoller H.-U., Eiden L.E., Herbert E., Grimes M.;
RT "Bovine chromogranin A sequence and distribution of its messenger RNA
RT in endocrine tissues.";
RL Nature 323:82-86(1986).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=87260925; PubMed=3474638;
RA Alm T.G., Conn D.V., Gott S.U., Ornstein D.L., Kashdan M.A.,
RA Levine M.A.;
RT "Primary structure of bovine pituitary secretory protein I
RT (chromogranin A) deduced from the cDNA sequence.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:5043-5047(1987).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=9728583; PubMed=9074643;
RA Kang Y.K., Yoo S.H.;
RT "Identification of the secretory vesicle membrane binding region of
RT chromogranin A.";
RL FEBS Lett. 404:87-90(1997).
RN [6]
RP SEQUENCE OF 19-45, AND CALCIUM-BINDING.
RX MEDLINE=90354431; PubMed=2387861;
RA Yoo S.H., Alameel U.P.;
RT "Ca2(+)-induced conformational change and aggregation of chromogranin
RT A.";
RL J. Biol. Chem. 265:14414-14421(1990).
RN [7]
RP SEQUENCE OF 142-161, AND SYNTHESIS OF CHROMOSTATIN.
RX MEDLINE=91143185; PubMed=1996343;
RA Galindo E., Rill A., Bader M.-F., Aunis D.;
RT "Chromostatin, a 20-amino acid peptide derived from chromogranin A,
RT inhibits chromaffin cell secretion.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:1426-1430(1991).
RN [8]
RP ERRATUM.
RA Galindo E., Rill A., Bader M.-F., Aunis D.;
RL Proc. Natl. Acad. Sci. U.S.A. 91:832-832(1994).

RN [9]
RP SEQUENCE OF 266-312.
RX MEDLINE=89331945; PubMed=2756155;
RA Nakano I., Funakoshi A., Miyasaka K., Ishida K., Maki G., Angwin P.,
RA Chang D., Tatemoto K.;
RT "Isolation and characterization of bovine pancreastatin.";
RL Regul. Pept. 25:207-213(1989).
RN [10]
RP SEQUENCE OF 191-212 (CHROMACIN), PHOSPHORYLATION SITE SER-191, AND
RP O-GLYCOSYLATION OF SER-204.
RX TISSUE=Chromaffin granules;
RX MEDLINE=97067080; PubMed=8910482;
RA Strub J.-M., Goumon Y., Lugardon K., Capon C., Lopez M., Moniatte M.,
RA van Dorsselaer A., Aunis D., Metz-Boutigue M.-H.;
RT "Antibacterial activity of glycosylated and phosphorylated
RT chromogranin A-derived peptide 173-194 from bovine adrenal medullary
RT chromaffin granules.";
RL J. Biol. Chem. 271:28533-28540(1996).
RN [11]
RP CHARACTERIZATION OF CATESTATIN.
RX MEDLINE=97439785; PubMed=9294131;
RA Mahata S.K., O'Connor D.T., Mahata M., Yoo S.H., Taupenot L., Wu H.,
RA Gill B.M., Farmer R.J.;
RT "Novel autocrine feedback control of catecholamine release. A discrete
RT antagonist.";
RL J. Clin. Invest. 100:1623-1633(1997).
RN [12]
RP CHARACTERIZATION OF CATESTATIN.
RX MEDLINE=99000113; PubMed=9786174;
RA Kennedy B.P., Mahata S.K., O'Connor D.T., Ziegler M.G.;
RT "Mechanism of cardiovascular actions of the chromogranin A fragment
RT catestatin in vivo.";
RL Peptides 19:1241-1248(1998).
RN [13]
RP 3D-STRUCTURE MODELING OF CATESTATIN.
RX MEDLINE=99025667; PubMed=9809795;
RA Tsigalou I., Mahata S.K., Taupenot L., Preece N.E., Mahata M.,
RA Khan I., Farmer R.J., O'Connor D.T.;
RT "Mechanism of action of chromogranin A on catecholamine release:
RT molecular modeling of the catestatin region reveals a beta-
RT strand/loop/beta-strand structure secured by hydrophobic interactions
RT and predictive of activity.";
RL Regul. Pept. 77:43-53(1998).
RN [14]
RP CHARACTERIZATION OF VASOSTATIN-1.
RX MEDLINE=20219105; PubMed=1075365;
RA Lugardon K., Raffner R., Goumon Y., Corti A., Delmas A., Bulet P.,
RA Aunis D., Metz-Boutigue M.-H.;
RT "Antibacterial and antifungal activities of vasostatin-1, the N-
RT terminal fragment of chromogranin A.";
RL J. Biol. Chem. 275:10745-10753(2000).
RN [15]
RP CARBOHYDRATE-LINKAGE SITES, PHOSPHORYLATION, AND DISULFIDE BOND.
RX MEDLINE=99459228; PubMed=10527498;
RA Bauer S.H., Zhang X.Y., Van Dongen W., Claessens M., Przybylski M.;
RT "Chromogranin A from bovine adrenal medulla: molecular
RT characterization of glycosylations, phosphorylations, and sequence
RT heterogeneity by mass spectrometry.";
RL Anal. Biochem. 274:69-80(1999).
RN [16]
RP FUNCTION: Pancreastatin strongly inhibits glucose induced insulin
RP release from the pancreas.
CC -1- FUNCTION: Chromostatin completely inhibits catecholamine release
CC from chromaffin cells.
CC -1- FUNCTION: Chromacin has antibacterial activity against M. luteus.
CC NOT active against E. coli.
CC -1- FUNCTION: Catestatin inhibits catecholamine release from
CC chromaffin cells and noradrenergic neurons by acting as a non-
CC competitive nicotinic cholinergic antagonist.
CC -1- FUNCTION: Vasoactive-1 has antibacterial activity against Gram-
CC positive bacteria M. luteus, B. megaterium. Not active against Gram-
CC positive bacteria B. cereus, B. subtilis, S. pyogenes, M. fortuitum,
CC S. aureus and L. monocytogenes and against Gram-negative bacteria

CC E.coli, E. cloacae, S. typhimurium, K. pneumoniae and P. aeruginosa.
 CC Possesses antifungal activity against N. crassa, A. fumigatus,
 CC A. brassicicola, N. hematozoa, F. culmorum and F. oxysporum and
 CC against S. cerevisiae and C. albicans yeast. Inactive against
 CC T. mentagrophytes.
 CC SUBCELLULAR LOCATION: Neuroendocrine and endocrine secretory
 CC granules.
 CC MASS SPECTROMETRY: MW=8584.9; METHOD=MALDI; RANGE=19-94.
 CC MISCELLANEOUS: Binds calcium with a low-affinity.
 CC SIMILARITY: BELONGS TO THE CHROMOGHRANIN / SECRETOGHRANIN PROTEIN
 CC FAMILY.
 CC -----
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 CC -----
 CC EMBL: S79270; AAB21297.1; JOINED.
 CC EMBL: S79256; AAB21297.1; JOINED.
 CC EMBL: S79253; AAB21297.1; JOINED.
 CC EMBL: S79260; AAB21297.1; JOINED.
 CC EMBL: S79262; AAB21297.1; JOINED.
 CC EMBL: S79264; AAB21297.1; JOINED.
 CC EMBL: S79266; AAB21297.1; JOINED.
 CC EMBL: S79268; AAB21297.1; JOINED.
 CC EMBL: X04012; CAA27636.1; JOINED.
 CC EMBL: X04012; CAA27636.1; JOINED.
 CC EMBL: M16971; AAA30765.1; JOINED.
 CC EMBL: U73523; AAC48700.1; JOINED.
 CC PIR: A41520; A41520.
 CC PDB: 1CFK; 22-MAR-99.
 CC PDB: 1NZY; 13-NOV-02.
 CC GlycoSuiteDB: P05059; Chromogranin_AB.
 CC InterPro: IPR001819; Chromogranin_AB.
 CC InterPro: IPR001990; Granin.
 CC Pfam: PF01271; Granin; 1.
 CC PRINTS: PR00659; CHROMOGRANIN.
 CC PROSITE: PS00422; CHROMOGRANIN.
 CC PROSITE: PS00423; GRANINS_2; 1.
 CC Signal: Amidation; Glycoprotein; Calcium-binding; Phosphorylation;
 CC Polymorphism; 3D-structure; Antibiotic; Fungicide.
 CC FT SIGNAL 1 18
 CC FT CHAIN 1 449 CHROMOGRANIN A.
 CC FT PEPTIDE 19 94 VASOSTATIN-1.
 CC FT PEPTIDE 142 161 CHROMOGRANIN.
 CC FT PEPTIDE 191 212 CHROMOGRANIN.
 CC FT PEPTIDE 266 312 PANCREASTATIN.
 CC FT PEPTIDE 334 347 WE-14.
 CC FT PEPTIDE 362 382 CATESTATIN.
 CC FT MOD_RES 99 99 PHOSPHORYLATION (PARTIAL).
 CC FT MOD_RES 142 142 PHOSPHORYLATION (PARTIAL).
 CC FT MOD_RES 191 191 PHOSPHORYLATION (PARTIAL).
 CC FT MOD_RES 315 315 PHOSPHORYLATION (PARTIAL).
 CC FT MOD_RES 350 350 PHOSPHORYLATION.
 CC FT MOD_RES 350 350 PHOSPHORYLATION.
 CC Query Match Score 37; DB 1; Length 449;
 CC Best Local Similarity 42.9%; Pred. No. 18;
 CC Matches 9; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Atrial natriuretic peptide clearance receptor precursor (ANP-C)
 DE (ANP-C) (Atrial natriuretic peptide C-type receptor) (EF-2).
 CN NP3.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 CC NCBI_Taxid=10090;
 RN (1)
 RN SEQUENCE FROM N.A.
 RC STRAIN=BALB/c; TISSUE=Lung;
 RX MEDLINE=96203905; PubMed=8620881;
 RA Yanaka N., Kotera J., Taguchi I., Sugiyama M., Kawashima K., Omori K.;
 RT "Structure of the 5'-flanking regulatory region of the mouse gene
 RL encoding the clearance receptor for atrial natriuretic peptide.";
 RL Eur. J. Biochem. 237:25-34(1996).
 RN (2)
 RN SEQUENCE FROM N.A., AND VARIANTS LGJ ASN-168 AND LGJ-2J ARG-66--SER-77
 RP DEL.
 RC STRAIN=BALB/c, and 129/Sv;
 RX MEDLINE=99398699; PubMed=10468599;
 RA Jambert J., Jambert F., Martin N., Washburn L.L., Lee B.K.,
 RT Elcher E.M., Guenet J.-L.;
 RT "Three new allelic mouse mutations that cause skeletal overgrowth
 RL involve the natriuretic peptide receptor C gene (Npr3)."
 RL Proc. Natl. Acad. Sci. U.S.A. 96:10278-10283(1999).
 RN (3)
 RN SEQUENCE OF 255-439 FROM N.A.
 RX MEDLINE=97184476; PubMed=9032278;
 RA Fu X., Kamps M.P.;
 RT "E2A-Pbx1 induces aberrant expression of tissue-specific and
 RT developmentally regulated genes when expressed in NIH 3T3
 RT fibroblasts.";
 RL Mol. Cell. Biol. 17:1503-1512(1997).
 RL (1)
 CC FUNCTION: RECEPTOR FOR ATRIAL NATRIURETIC PEPTIDE. DOES NOT HAVE
 CC GUNYATE CYCLASE ACTIVITY.
 CC -1- SUBUNIT: Homodimer; disulfide-linked (by similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- DISEASE: Defects in NP3 are the cause of a number of skeletal-
 CC overgrowth phenotypes, Longjohn (lgj), longjohn-2j (lgj-2j) and
 CC Strigosus (Stri). These are all recessive conditions characterized
 CC by an elongated body, thoracic kyphosis, archednecly, and
 CC sacral and/or tail kinks, but no significant changes in
 CC craniofacial structures.
 CC -1- MISCELLANEOUS: THERE SEEM TO BE AT LEAST THREE ANP RECEPTORS: TWO
 CC WITH GUNYATE CYCLASE ACTIVITY (ANP-A AND ANP-B) AND ONE (ANP-C)
 CC WHICH IS PROBABLY RESPONSIBLE FOR THE CLEARANCE OF ANP FROM THE
 CC CIRCULATION WITHOUT A ROLE IN SIGNAL TRANSDUCTION.
 CC -1- SIMILARITY: TO ANP-A AND ANP-B RECEPTOR IN THEIR EXTRACELLULAR AND
 CC TRANSMEMBRANE DOMAINS.
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 CC -----
 CC EMBL: D78175; BA011241.1; JOINED.
 CC EMBL: AF131861; AF001014.1; JOINED.
 CC EMBL: AF131862; AF001015.1; JOINED.
 CC EMBL: AF131864; AF001017.1; JOINED.
 CC EMBL: U72676; AAB51036.1; JOINED.
 CC PIR: S71332; S71332.
 CC MGI: 97373; Npr3.
 CC InterPro: IPR001828; ANP receptor.
 CC InterPro: IPR001170; Ntpep receptor.
 CC Pfam: PF01094; ANP_receptor; 1.
 CC PRINTS: PR00255; NATPEPTIDER.
 CC PROSITE: PS00458; ANP_RECEPTORS; 1.
 CC Receptor; Glycoprotein; Transmembrane; Signal.
 CC FT SIGNAL 1 26
 CC FT POTENTIAL.


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FT PROPEP 27 40 POTENTIAL.
FT CHAIN 41 536 ATRIAL NATRIURETIC PEPTIDE CLEARANCE
FT TRANSMEM 41 498 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 479 499 POTENTIAL.
FT DISULFID 500 536 CYTOPLASMIC (POTENTIAL).
FT DISULFID 103 131 BY SIMILARITY.
FT DISULFID 208 256 INTERCHAIN (BY SIMILARITY).
FT DISULFID 468 468 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 81 81 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 288 389 MISSING (IN LGF-20).
FT VARIANT 66 77 H -> N (IN LGU).
FT VARIANT 168 168 DS -> IT (IN REF. 1).
FT VARIANT 58 59 E -> G (IN REF. 1).
FT CONFLICT 132 132 G -> V (IN REF. 3).
FT CONFLICT 293 293 Y -> C (IN REF. 3).
FT CONFLICT 348 348
FT CONFLICT 348 348
SQ SEQUENCE 536 AA; 59841 MW; 22E14B5C454F4427 CRC64;

Query Match 33.0%; Score 37; DB 1; Length 536;
Best Local Similarity 56.2%; Pred. No. 22;
Matches 9; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 19 VRLXXXXXGXSSGA 34
DB 13 VLLARVLLAGGASSGA 28

RESULT 10
VU79_HSV6U STANDARD; PRT; 344 AA.
AC P52528;
DC 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein U79.
GN U79 OR EDRF1.
OS Human herpesvirus (type 6 / strain Uganda-1102) (HHV6).
OC Herpesviridae; Herpesvirinae; no RNA stage; Herpesviridae;
OC Betaherpesvirinae; Roseolovirinae.
OC NCBI_TaxID=10370;
OX
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=95027704; Pubmed=7941342;
RA Nicholas J.;
RT "Nucleotide sequence analysis of a 21-kbp region of the genome of human herpesvirus-6 containing homologues of human cytomegalovirus major immediate-early and replication genes."
RL Virology 204:738-750(1994).
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=95266321; Pubmed=7747482;
RA Compels U.A., Nicholas J., Lawrence G., Jones M., Thomson B.U.,
RA Martin M.E., Efthahiou S., Craxton M., Macaulay H.A.;
RT "The DNA sequence of human herpesvirus-6: structure, coding content, and genome evolution."
RL Virology 209:29-51(1995).
CC -1- FUNCTION: POSSIBLE REPLICATION PROTEIN.
CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUP TOGETHER HSV-6 AND
CC HSV-7 U79 AND HCMV UL112 (P34).
CC
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CC -----
DR EMBL; U13194; AAA68470.1; -
DR EMBL; X83413; CAA58371.1; -
DR InterPro; IPR004138; U79_P34.

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DR Pfam; PF03064; U79_P34.1;
SQ SEQUENCE 344 AA; 39272 MW; E34F1F7ADB7D790 CRC64;

Query Match 32.1%; Score 36; DB 1; Length 344;
Best Local Similarity 30.4%; Pred. No. 22;
Matches 7; Conservative 3; Mismatches 13; Indels 0; Gaps 0;

QY 12 KQEEAVRLXXXXXGXSSGA 34
DB 261 EQSHEDGTLTSTLVNGAVBGA 283

RESULT 11
SP4_HUMAN STANDARD; PRT; 784 AA.
ID Q02446; O60402;
AC Q02446; O60402;
DC 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Transcription factor Sp4 (SP4-1).
GN SP4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
OX
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=93087156; Pubmed=1454515;
RA Hagen G., Mueller S., Beato M., Suske G.;
RT "Cloning by recognition site screening of two novel GT box binding
RT proteins: a family of Sp1 related genes."
RL Nucleic Acids Res. 20:5519-5525(1992).
RN
RP SEQUENCE FROM N.A.
RA Ozeresky P., Holmes A.;
RT Submitted (Apr-1998) to the EMBL/GenBank/DBJ databases.
CC
CC -1- FUNCTION: Binds to GT and GC boxes promoters elements. Probable
CC transcriptional activator.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- TISSUE SPECIFICITY: ABUNDANT IN BRAIN.
CC -1- SIMILARITY: BELONGS TO THE SP1 FAMILY OF C/EBP-TYPE ZINC-FINGER
CC PROTEINS.
CC
CC -1- SIMILARITY: Contains 3 C/EBP-type zinc fingers.
CC
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CC -----
DR EMBL; X68561; CAA48563.1; -
DR EMBL; AC004595; AAD12226.1; -
DR PIR; S26638; S26638.
DR HSSP; P08047; 1SP1.
DR TRANSFAC; T02339; -
DR GeneW; HGNC:11209; SP4.
DR MIM; 600540; -
DR GO; GO:0003702; F:RNA polymerase II transcription factor acti. . .; TAS.
DR GO; GO:0003713; F:transcription co-activator activity; TAS.
DR GO; GO:0006357; P:regulation of transcription from Pol II pro. . .; TAS.
DR InterPro; IPR007087; Znf C/EBP.
DR Pfam; PF00096; zfc_C/EBP; 3.
DR ProDom; PD000003; Znf C/EBP; 2.
DR SMART; SM00355; ZNF_C/EBP; 3.
DR PROSITE; PS00028; ZINC_FINGER_C/EBP; 3.
DR PROSITE; PS50157; ZINC_FINGER_C/EBP; 3.
KM Transcription regulation; Activator; Zinc-finger; Metal-binding;
KM DNA-binding; Nuclear protein; Repeat.
FT ZN_FING 647 671 C/EBP-TYPE 1.
FT ZN_FING 677 701 C/EBP-TYPE 2.

```

Query Match 32.1%; Score 36; DB 1; Length 784;
 Best Local Similarity 29.2%; Pred. No. 51;
 Matches 8; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

12 KXEEBAVRLXXXXXGXSS 32
 6 KEEEBAAAAAAMATEGKTS 26

RESULT 12
 ID NUC1 NEUCR STANDARD; PRT; 823 AA.
 AC P20824;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Phosphorus acquisition controlling protein.
 GN NUC-1.
 OS Neurospora crassa.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
 OX NCBI_TaxID=5141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=40-21; PubMed=2146493;
 RX MEDLINE=91042513; PubMed=2146493;
 RA Kang S., Metzberg R.L.;
 RT "Molecular analysis of nuc-1+, a gene controlling phosphorus
 acquisition in Neurospora crassa."
 RT Mol. Cell. Biol. 10:5839-5848(1990).
 CC -1- FUNCTION: FACTOR THAT ACTIVATES THE TRANSCRIPTION OF STRUCTURAL
 CC GENES FOR PHOSPHORUS ACQUISITION.
 CC -1- SUBUNIT: Binds DNA as a dimer.
 CC -1- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
 CC TRANSCRIPTION FACTORS.
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 CC
 DR EMBL: M37700; AAA3603.1; -
 DR PIR: A36378; A36378.
 DR HSSP: P07270; 1A0A.
 DR TRANSFAC: T01642; -
 DR InterPro: IPR001092; HLH_basic.
 DR Pfam: PF00010; HLH_1.
 DR SMART: SM00353; HLH_1.
 DR PROSITE: PS00038; HLH_1; 1.
 DR PROSITE: PS00888; HLH_2; 1.
 KM DNA-binding; Transcription regulation; Nuclear protein; Activator.
 FT DOMAIN 22 51
 FT DOMAIN 101 220
 FT DOMAIN 434 556
 FT DOMAIN 468 562
 FT DOMAIN 718 758
 FT SEQUENCE 823 AA; 87275 MW; 55513ED9896652F CRC64;

Query Match 32.1%; Score 36; DB 1; Length 823;
 Best Local Similarity 29.2%; Pred. No. 54;
 Matches 7; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

11 SKXEEBAVRLXXXXXGXSSGA 34
 765 NKRAEBAERKLVEMKOGGATGS 788

RESULT 13

ID CARB SULFO STANDARD; PRT; 1049 AA.

AC 0970U7;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Carboxyl-phosphate synthase large chain (EC 6.3.5.5) (Carboxyl-
 DE phosphate synthase ammonia chain).
 GN CARB OR ST1504.
 OS Sulfolobus tokodaii.
 OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
 OC Sulfolobus.
 OX NCBI_TaxID=111955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=JCM 10545 / 7;
 RX MEDLINE=21456156; PubMed=11572479;
 RA Kawarabayashi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
 RA Sekine M., Baba S.-I., Anka A., Kosugi H., Hosoyama A., Fukui S.,
 RA Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamaya M., Kato Y.,
 RA Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
 RA Aoki K.-I., Masuda S., Yanagi M., Nishimura M., Yamagishi A.,
 RA Oshima T., Kikuchi H.;
 RT "Complete genome sequence of an aerobic thermophilic
 RT Crenarchaeon, Sulfolobus tokodaii strain";
 RT DNA Res. 8:123-140(2001).
 CC -1- CATALYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP +
 CC phosphate + L-glutamate + carbamoyl phosphate.
 CC -1- COFACTOR: Binds 3 manganese ions per subunit (By similarity).
 CC -1- PATHWAY: Arginine biosynthesis, first step.
 CC -1- PATHWAY: Pyrimidine biosynthesis, first step.
 CC -1- SUBUNIT: Composed of two chains, the small (or glutamine) chain
 CC promotes the hydrolysis of glutamine to ammonia, which is used by
 CC the large (or ammonia) chain to synthesize carbamoyl phosphate (By
 CC similarity).

-1- SIMILARITY: BELONGS TO THE CARB FAMILY.

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 or send an email to license@isb-sib.ch).

DR EMBL: AP000966; BA866576.1; -
 DR HAMAP: MF_01210; - 1.
 DR InterPro: IPR006275; CARB_L_glu.
 DR InterPro: IPR005483; Cpsase_L.
 DR InterPro: IPR005479; Cpsase_L_D2.
 DR InterPro: IPR005480; Cpsase_L_D3.
 DR InterPro: IPR005481; Cpsase_L_N.
 DR Pfam: PF00289; Cpsase_L_chain_2.
 DR Pfam: PF02786; Cpsase_L_D2; 2.
 DR Pfam: PF02787; Cpsase_L_D3; 1.
 DR PRINTS: PR00098; Cpsase.
 DR TIGRFAMs: TIGR01369; CpsaseII_1fg; 1.
 DR PROSITE: PS00867; Cpsase_2; 1.
 DR PROSITE: PS00865; Cpsase_1; 1.
 KM Arginine biosynthesis; Pyrimidine biosynthesis; Ligase; Repeat;
 KM ATP-binding; Manganese; Complete proteome.
 FT DOMAIN 1 399
 FT DOMAIN 400 548
 FT OLIGOMERIZATION DOMAIN.

FT DOMAIN 549 930 CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.
 FT DOMAIN 931 1049 ALLOSTERIC DOMAIN.
 FT REPEAT 1 548
 FT REPEAT 549 1049
 FT NP_BIND 151 208 ATP (POTENTIAL).
 FT NP_BIND 300 350 ATP (POTENTIAL).
 FT METAL 282 282 MANGANESE 1 (BY SIMILARITY).
 FT METAL 296 296 MANGANESE 1 AND 2 (BY SIMILARITY).
 FT METAL 298 298 MANGANESE 2 (BY SIMILARITY).
 FT METAL 823 823 MANGANESE 3 (BY SIMILARITY).
 FT METAL 835 835 MANGANESE 3 (BY SIMILARITY).
 SQ SEQUENCE 1049 AA; 117504 MW; 41FB5EF1A1F94AF CRC64;

Query Match 32.1%; Score 36; DB 1; Length 1049;
 Best Local Similarity 63.6%; Pred. No. 70;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 11 SKXEEBAYRL 21
 11 SKXEEBAYRL 21
 646 SKLEBEGRL 656

Db 646 SKLEBEGRL 656

RESULT 14
 POLG_PEMVC STANDARD; PRT; 3068 AA.
 ID POLG_PEMVC
 AC 001500;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Genome polypeptide (Contains: N-terminal protein (P1); Helper
 component polypeptide (HC-Pro); Protein P3; 6 kDa
 protein 1 (6K2); Cytoplasmic inclusion protein (CI); 6 kDa protein 2
 (6K2); Genome-linked protein (VPO); Nuclear inclusion protein A (N1-A)
 (N1A) (EC 3.4.22.44) (49 kDa proteinase) (49 kDa-Pro); Nuclear
 inclusion protein B (N1-B) (N1B) (RNA-directed RNA polymerase)
 (EC 2.7.7.48); Coat protein (CP) 1.
 DE Pepper mottle virus (California isolate) (PemoV) (PemoV C).
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
 OC Potyvirus.
 OC NCBI_taxid=31737;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9303110; PubMed=1413501;
 RA Vance V.B., Moore D., Turpen T.H., Bracker A., Hollwell V.C.;
 RT "The complete nucleotide sequence of pepper mottle virus genomic RNA:
 comparison of the encoded polypeptide with those of other sequenced
 potyviruses";
 RT potyvirus.
 RT Virology 191:19-30(1992).
 RL Virology 191:19-30(1992).
 CC -1- FUNCTION: HELPER COMPONENT-PROTEINASE IS REQUIRED FOR APHID
 TRANSMISSION AND ALSO HAS PROTEOLYTIC ACTIVITY.
 CC -1- FUNCTION: CYTOPLASMIC INCLUSION PROTEIN HAS HELICASE ACTIVITY. IT
 MAY BE INVOLVED IN REPLICATION.
 CC -1- FUNCTION: NUCLEAR INCLUSION PROTEIN A HAS PROTEOLYTIC ACTIVITY.
 CC -1- CATALYTIC ACTIVITY: Hydrolyzes glutamyl bonds, and activity is
 further restricted by preferences for the amino acids in P6-P1
 that vary with the species of potyvirus, e.g. Glu-Xaa-Xaa-Tyr-Xaa-
 Gln(Ser or Gly) for the enzyme from tobacco etch virus. The
 natural substrate is the viral polypeptide, but other proteins and
 oligopeptides containing the appropriate consensus sequence are
 also cleaved.
 CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
 (RNA)(N).
 CC -1- CATALYTIC ACTIVITY: Hydrolyzes a Gly-I-Gly bond at its own C-
 terminus, commonly in the sequence -Tyr-Xaa-Val-Gly-I-Gly, in the
 processing of the polyviral polypeptide.
 CC -1- PM: VPG IS COVALENTLY LINKED TO THE GENOMIC RNA.
 CC -1- PM: THE VIRAL RNA OF POTYVIRUS IS EXPRESSED AS A SINGLE
 POLYPEPTIDE WHICH UNDERGOES POSTTRANSLATIONAL PROTEOLYTIC
 PROCESSING RESULTING IN THE PRODUCTION OF AT LEAST EIGHT
 INDIVIDUAL PROTEINS.
 CC -1- SIMILARITY: HC PROTEINASE BELONGS TO PEPTIDASE FAMILY C6.
 CC -1- SIMILARITY: N1-A PROTEINASE BELONGS TO PEPTIDASE FAMILY C4.
 CC -1- SIMILARITY: BELONGS TO THE POTYVIRUS POLYPEPTIDE FAMILY.

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 CC -----
 CC EMBL, M96425; AAA46903.1; -;
 CC PIR, A44062; A44062.
 CC MEROPS, C04.002; -;
 CC MEROPS, C06.001; -;
 CC MEROPS, S30.001; -;
 CC InterPro: IPR001410; DEAD.
 CC InterPro: IPR001650; Helicase_C.
 CC InterPro: IPR001730; Peptidase_C4.
 CC InterPro: IPR001456; Peptidase_C6.
 CC InterPro: IPR001592; Pcty_coat.
 CC InterPro: IPR002540; Pcty_P1.
 CC InterPro: IPR007095; RNA_pol_DS_PS.
 CC InterPro: IPR001205; RNA_pol_P3D.
 CC InterPro: IPR007094; RNA_pol_PSVir.
 CC Pfam: PF00270; DEAD; 1.
 CC Pfam: PF00271; Helicase_C; 1.
 CC Pfam: PF00863; Peptidase_C4; 1.
 CC Pfam: PF00851; Peptidase_C6; 1.
 CC Pfam: PF00767; Pcty_coat; 1.
 CC Pfam: PF01577; Pcty_P1; 1.
 CC Pfam: PF00680; RNA_dep_RNA_pol; 1.
 CC PRINTS: PR00966; N1A/POTYPITASE.
 CC SMART: SM00487; DEXDC; 1.
 CC SMART: SM00490; HELIC; 1.
 CC KX Helicase; Transferrase; Thiol protease; RNA-directed RNA polymerase;
 CC KM Coat protein; Polypeptide; Covalent protein-RNA linkage; Helicase;
 CC KW ATP-binding.
 CC FT CHAIN 1 287 N-TERMINAL PROTEIN.
 CC FT CHAIN 288 743 HELPER COMPONENT PROTEINASE.
 CC FT CHAIN 744 ? PROTEIN P3.
 CC FT CHAIN ? 1156 6 kDa protein 1.
 CC FT CHAIN 1157 1790 CYTOPLASMIC INCLUSION PROTEIN.
 CC FT CHAIN 1791 1842 6 kDa protein 2.
 CC FT CHAIN 1843 ? GENOME-LINKED PROTEIN.
 CC FT CHAIN ? 2276 NUCLEAR INCLUSION PROTEIN A.
 CC FT CHAIN 2277 2795 NUCLEAR INCLUSION PROTEIN B.
 CC FT CHAIN 2796 3068 COAT PROTEIN.
 CC FT BINDING 1906 1906 COVALENT LINKAGE OF VIRAL RNA
 CC (BY SIMILARITY).
 FT NP_BIND 1241 1248 ATP (POTENTIAL).
 SQ SEQUENCE 3068 AA; 348651 MW; FD345B837FDA7C2 CRC64;

Query Match 32.1%; Score 36; DB 1; Length 3068;
 Best Local Similarity 80.0%; Pred. No. 2; 2e+02;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 12 KXEEBAYRL 21
 12 KXEEBAYRL 21
 87 KXEEBAYRL 96

Db 87 KXEEBAYRL 96

RESULT 15
 FTSZ_BACSU STANDARD; PRT; 382 AA.
 ID FTSZ_BACSU
 AC P17865;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cell division protein ftsZ.
 OS Bacillus subtilis.
 OS Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OC NCBI_taxid=1423;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=89008108; PubMed=3139638;
 RT Beall B., Lowe M., Lutkenhaus J.,
 RT "Cloning and characterization of *Bacillus subtilis* homologs of
 RT *Escherichia coli* cell division genes *ftsZ* and *ftsA*,"
 RL J. Bacteriol. 170:4855-4864(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RC MEDLINE=98044033; PubMed=9384377;
 RA Kunst F., Ogatawara N., Moser I., Albertini A.M., Alloni G.,
 RA Azevedo V., Betteiro M.G., Bessieres P., Bolotin A., Borchert S.,
 RA Borris R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
 RA Brouillet S., Bruschi C.V., Caldwell J., Capuano N.J., Carter N.M.,
 RA Choi S.K., Codani J.J., Conerton I.F., Cummings N.J., Daniel R.A.,
 RA Denizot F., Devine K.M., Dusterhoft A., Enright S.D., Emerson P.T.,
 RA Enright K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
 RA Fritze C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
 RA Gilm S.Y., Glaeser P., Goltz A., Goltz E.J., Grandi G.,
 RA Giuseppe G., Guy B.J., Haga K., Haeck J., Harwood C.R., Henaut A.,
 RA Hilbert H., Holstappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
 RA Joris B., Karamata D., Kasahara Y., Klier-Blanchard M., Klein C.,
 RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
 RA Kurita K., Lapilus A., Lardinois S., Lauber J., Lazarevic V.,
 RA Lee S.M., Levine A., Liu H., Masuda S., Manuel C., Medigue C.,
 RA Medina N., Melillo R.P., Mizuno M., Moser I., Nakai S., Noback M.,
 RA Noone D., O'Reilly M., Ogawa K., Ogatawara N., Oudega B., Park S.H.,
 RA Paro V., Pohl T.M., Portetle D., Potwolik S., Prescott A.M.,
 RA Preece E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
 RA Rieger M., Rivolta E., Rochet S., Roche B., Rose M., Sadie Y.,
 RA Sato T., Scanlan E., Schleich S., Schroeter R., Scofield F.,
 RA Sekiguchi J., Sekowska A., Serrif S.J., Serrif P., Shin B.S., Soldo B.,
 RA Sorek N., Taconi E., Takagi T., Takahashi H., Takemaru K.,
 RA Takeuchi M., Tanakoshi A., Tanaka T., Terpetra P., Tognoni A.,
 RA Tosiato V., Uchiyama S., Vandenbol M., Vannier F., Vassatoti A.,
 RA Viari A., Wambut R., Wedler E., Wedler H., Weitzenecker T.,
 RA Witters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
 RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.,
 RA "The complete genome sequence of the Gram-positive bacterium *Bacillus*
 RT *subtilis*,"
 RT Nature 390:249-256(1997).
 RN [3]
 RP SEQUENCE OF 371-382 FROM N.A.
 RX MEDLINE=90216713; PubMed=2108961;
 RA Mu X.-C., Nathoo S., Pang A.S.-H., Carne T., Wang S.-L.,
 RT "Cloning, genetic organization, and characterization of a structural
 RT gene encoding bacillopeptidase F from *Bacillus subtilis*,"
 RL J. Biol. Chem. 265:6845-6850(1990).
 CC -1- FUNCTION: This protein is essential to the cell-division process.
 CC It seems to assemble into a dynamic ring on the inner surface of
 CC the cytoplasmic membrane at the place where division will occur,
 CC and the formation of the ring is the signal for septation to
 CC begin. Binds to and hydrolyzes GTP (By similarity).
 CC -1- SUBUNIT: Aggregates to form a ring-like structure (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic. Assembles at the inner surface
 CC of the cytoplasmic membrane (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE FTSZ FAMILY.
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 CC EMBL, M22630; AAA22457.1; -
 CC EMBL, Z99111; CAB13402.1; -
 CC EMBL, J05400; AAA83361.1; -
 CC PIR, I39848; I39848.
 CC HSP, Q57816; IFSZ.
 CC Subtilist; BG10232; ftsZ.
 CC InterPro; IPR000158; ftsZ.

DR InterPro; IPR003008; Tubulin_FtsZ.
 DR Pfam; PF00091; tubulin.1.
 DR Pfam; PF03953; tubulin.C.1.
 DR PRINTS; PR00423; CEMLDVIFSTZ.
 DR TIGFAMS; TIGR00065; ftsZ.1.
 DR PROSITE; PS01134; FTSZ_1; 1.
 DR PROSITE; PS01135; FTSZ_2; 1.
 KM Cell division; Septation; GTP-binding; Complete proteome.
 NP BIND 104 112
 SC SEQUENCE 362 AA; 4035 MW; D1E908DED2734C8B CRC64;
 Query Match 31.7%; Score 35.5; DB 1; Length 382;
 Best Local Similarity 27.8%; Pred. No. 30;
 Matches 10; Conservative 5; Mismatches 16; Indels 5; Gaps 1;
 QY 4 GTXXXXXSKXEEFVNR-----LXXXXLXGXSSGA 34
 DB 78 GKAAEESKEQIEALKGADNVFVYAGMGSGTGTGA 113
 RESULT 16
 TF2B, PYRAB
 ID TF2B, PYRAB STANDARD; PRT; 300 AA.
 AC Q9V0V5;
 DT 16-OCT-2001 (Rel. 40; Created)
 DT 16-OCT-2001 (Rel. 40; Last sequence update)
 DT 15-SEP-2003 (Rel. 42; Last annotation update)
 DE Transcription initiation factor IIB (TFIIB).
 GN TFB OR PYRAB06850 OR PAB1912.
 OS Pyrococcus abyssi.
 OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
 OC Pyrococcus.
 NC NCBI_TaxID=29292;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GES / Orsay;
 RX PubMed=12622808;
 RA Cohen G.N., Barbe V., Flament D., Galperin M., Helling R., Lecompte O.,
 RA Foch O., Piteur D., Querrelou J., Ripp R., Thierry J.-C.,
 RA Van der Oost J., Weisenbach J., Zivanovic Y., Forterre P.;
 RT "An integrated analysis of the genome of the hyperthermophilic
 RT archaeon *Pyrococcus abyssi*,"
 RL Mol. Microbiol. 47:1495-1512(2003).
 CC -1- FUNCTION: STABILIZES TBP BINDING TO AN ARCHAEL BOX-A PROMOTER.
 CC ALSO RESPONSIBLE FOR RECRUITING RNA POLYMERASE II TO THE PRE-
 CC INITIATION COMPLEX (DNA-TBP-TFIIB) (By similarity).
 CC -1- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
 CC -1- SIMILARITY: Belongs to the TFIIB family.
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 CC EMBL; AJ248285; CAB49598.1; -
 DR PIR; E75110; E75110.
 DR HSP; P25095; IAI5.
 DR HAMAP; MF_00383; -1.
 DR InterPro; IPR006670; Cyclin.
 DR InterPro; IPR000812; TFIIB_euk.
 DR Pfam; PF00382; transcripTfac2.2.
 DR PRINTS; PR00685; TIFACTOR1IB.
 DR SMART; SW00385; CYCLIN; 2.
 DR PROSITE; PS00782; TFIIB; 2.
 KW Transcription regulation; Repeat; Zinc-finger; Metal-binding; Zinc;
 KW Complete proteome.
 FT ZN FING 7 29
 FT REPEAT 114 197
 FT REPEAT 210 291
 FT METAL 7 7
 FT ZINC (BY SIMILARITY).

FT METAL 10 10 ZINC (BY SIMILARITY).
 FT METAL 26 26 ZINC (BY SIMILARITY).
 FT METAL 29 29 ZINC (BY SIMILARITY).
 SQ SEQUENCE 300 AA; 34069 MW; D7AE15181A36BDF CRC64;
 Query Match 31.2%; Score 35; DB 1; Length 300;
 Best Local Similarity 40.9%; Pred. No. 29;
 Matches 9; Conservative 1; Mismatches 12; Indels 0; Gaps 0;
 QY 12 KQEEBAVLXXXXLXGXSSG 33
 DB 127 KHEEEAARLYREAVRKGLRG 148
 RESULT 17
 FT2B_PYRHO STANDARD; PRT; 300 AA.
 ID TF2B_PYRHO
 AC 059151;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Transcription initiation factor IIB (TFIIB).
 GN TFB OR PH1482
 OS Pyrococcus horikoshii
 OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
 OC Pyrococcus.
 NC NCB1_TaxID=53953;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CT3
 RX MEDLINE=9834437; PubMed=9679194;
 RA Kawarabayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
 RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
 RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamaya M., Ohtuku Y.,
 RA Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kishida N., Oguchi A.,
 RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
 RA Masuchi Y., Shizuya H., Kikuchi H.;
 RT "Complete sequence and gene organization of the genome of a hyper-
 thermophilic archaeobacterium, Pyrococcus horikoshii CT3.";
 RL DNA Res. 5:55-76(1998).
 CC -1- FUNCTION: STABILIZES TBP BINDING TO AN ARCHAEAL BOX-A PROMOTER.
 CC ALSO RESPONSIBLE FOR RECRUITING RNA POLYMERASE II TO THE PRE-
 CC INITIATION COMPLEX (DNA-TBP-TFIIB) (BY SIMILARITY).
 CC -1- CORCTOR: Binds 1 zinc ion per subunit (By similarity).
 CC -1- SIMILARITY: Belongs to the TFIIB family.
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 CC -----
 CC EMBL; APO00006; BAA30589.1; -
 CC PIR; E71023; E71023.
 CC HAMAP; P29035; 1A1S.
 CC HAMP; MF 00383; -; 1.
 CC InterPro; IPR006670; CycIin.
 CC InterPro; IPR000812; TFIIB_euk.
 CC Pfam; PF00382; Transcrip_Fac2; 2.
 CC PRINTS; PRO0685; TIFACTOR1B.
 CC SMART; SM00385; CYCLIN; 2.
 CC PROSITE; PS00782; TFIIB; 2.
 CC Transcription regulation; Repeat; Zinc-finger; Metal-binding; Zinc;
 CC Complete proteome.
 CC ZN FING 7 29
 FT REPEAT 114 197 ZN-R-BBOX TFIIB-TYPE.
 FT REPEAT 210 291 1.
 FT METAL 7 7 ZINC (BY SIMILARITY).
 FT METAL 10 10 ZINC (BY SIMILARITY).
 FT METAL 26 26 ZINC (BY SIMILARITY).
 FT METAL 29 29 ZINC (BY SIMILARITY).

SQ SEQUENCE 300 AA; 34097 MW; DE9758F398BC855F CRC64;
 Query Match 31.2%; Score 35; DB 1; Length 300;
 Best Local Similarity 40.9%; Pred. No. 29;
 Matches 9; Conservative 1; Mismatches 12; Indels 0; Gaps 0;
 QY 12 KQEEBAVLXXXXLXGXSSG 33
 DB 127 KHEEEAARLYREAVRKGLRG 148
 RESULT 18
 ID FLIG_PSEAE STANDARD; PRT; 338 AA.
 AC 051464;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Flagellar motor switch protein flig.
 GN FLIG OR PA1102.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 NC NCB1_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 15692 / PA01;
 RX MEDLINE=20437337; PubMed=10984043;
 RA Stover C.K., Pham X.-Q.T., Erwin A.L., Micozuchi S.D., Warren P.,
 RA Hickey M.J., Brinkman F.S.L., Huftagle W.O., Kowalik D.J., Lagrou M.,
 RA Gardner R.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
 RA Brody L.L., Coulter S.N., Folger K.R., Kae A., Larbig K., Lim R.M.,
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 RA Reizer J., Salter M.H., Hancock R.E.W., Lory S., Olson M.V.,
 RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
 RT opportunistic pathogen.";
 RL Nature 406:959-964(2000).
 CC [2]
 CC SEQUENCE OF 1-228 FROM N.A.
 CC STRAIN=PAK;
 CC MEDLINE=96239027; PubMed=8675317;
 CC Alora S.K., Ritchings B.W., Almira E.C., Lory S., Ramphal R.;
 CC "Cloning and characterization of Pseudomonas aeruginosa flig,"
 CC necessary for flagellar assembly and bacterial adherence to mucin.";
 CC Infect. Immun. 64:2130-2136(1996).
 CC -1- FUNCTION: FLIG IS ONE OF THREE PROTEINS (FLIG, FLIN, FLIM) THAT
 CC FORM A SWITCH COMPLEX THAT IS PROPOSED TO BE LOCATED AT THE BASE
 CC OF THE BASAL BODY. THIS COMPLEX INTERACTS WITH THE CHEV AND CHEZ
 CC CHEMOTAXIS PROTEINS, IN ADDITION TO CONTRACTING COMPONENTS OF THE
 CC MOTOR THAT DETERMINE THE DIRECTION OF FLAGELLAR ROTATION (BY
 CC SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Inner membrane-associated (Potential).
 CC -1- SIMILARITY: BELONGS TO THE FLIG FAMILY.
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 CC -----
 CC EMBL; AE004540; AAG04491.1; -
 CC PIR; L43507; AAB06802.1; -
 CC PIR; G83508; G83508.
 CC HSSP; G9WY63; 10C7.
 CC InterPro; IPR000090; Flg_Motor_Flig.
 CC Pfam; PF01706; Flig-C; 1.
 CC PRINTS; PR00954; FLGMOTORFLIG.
 CC TIGRFAMs; TIGR00207; Flig.1.
 CC Chemotaxis; Flagella; Flagellar rotation; Inner membrane;
 CC Complete proteome.
 CC SEQUENCE 338 AA; 37007 MW; 81BFB136B4D1FA1 CRC64;

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AE015476; AAN53363.1; -
CC TIGR; S00278; -
CC HAMAP; MF_00005; -; 1
CC InterPro; IPR001518; Argininosuc_synth.
CC Pfam; PF00764; Argininosuc_synth; 1
CC ProDom; PD003544; Argininosuc_synth; 1
CC TrEMBL; TIGR00032; argG; 1
CC PROSITE; PS00564; ARGININOSUCCIN SYN 1; 1
CC PROSITE; PS00565; ARGININOSUCCIN SYN 2; 1
CC Arginine biosynthesis; Ligase; ATP-binding; Complete proteome.
CC KW Arginine biosynthesis; Ligase; ATP-binding; Complete proteome.
CC SEQUENCE 407 AA; 44538 MW; ABCABCECE33E345 CRC64;

Query Match 31.2%; Score 35; DB 1; Length 407;
Best Local Similarity 42.1%; Pred. No. 40;
Matches 8; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 13 QXEEBRLXXXXXGXS 31
DB 48 QCEEBLIGLEKALSGAS 66

RESULT 21
ID IDS_MOUSE STANDARD; PRT; 563 AA.
AC Q08890;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
GN Iduronate 2-sulfatase precursor (EC 3.1.6.13).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Thymus;
RX MEDLINE=93315172; PubMed=8325651;
RT Daniel A., Faust C.U., Herman G.E., di Natale P., Ballabio A.;
RT "Cloning and characterization of the cDNA for the murine iduronate
RT sulfatase gene.";
RL Genomics 16:755-757(1993).
CC -1- FUNCTION: REQUIRED FOR THE LYSOSOMAL DEGRADATION OF HEPARAN
CC SULFATE AND DERMATAN SULFATE.
CC -1- CATALYTIC ACTIVITY: Hydrolysis of the 2-sulfate groups of the L-
CC iduronate 2-sulfate units of dermatan sulfate, heparan sulfate and
CC heparin.
CC -1- SUBCELLULAR LOCATION: Lysosomal.
CC -1- SIMILARITY: BELONGS TO THE SULFATASE FAMILY.

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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; L07921; AAA37880.1; -
CC PIR; A47153; A47153.
CC MGD; MGI:96417; Ids.
CC InterPro; IPR00917; Sulfatase.
CC Pfam; PF00884; Sulfatase; 1
CC PROSITE; PS00523; SULFATASE 1; 1
CC PROSITE; PS00149; SULFATASE 2; 1
CC Hydrolyase; Glycoprotein; Lysosome; Zymogen; Signal.
CC SIGNAL 1
CC PROPEP 59
CC CHAIN 60 563
CC MOD_RES 99 99 2-AMINO-3-OXOPROPIONIC ACID (BY

FT CARBOHYD 130 130
FT CARBOHYD 159 159
FT CARBOHYD 261 261
FT CARBOHYD 295 295
FT CARBOHYD 526 526
FT CARBOHYD 550 550
SQ SEQUENCE 563 AA; 63437 MW; 52D008F91BA88FAC CRC64;

Query Match 31.2%; Score 35; DB 1; Length 563;
Best Local Similarity 70.0%; Pred. No. 56;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 12 KXEEBRL 21
DB 214 KXEEBRL 223

RESULT 22
ID MKLN_HUMAN STANDARD; PRT; 735 AA.
AC Q9UL63; Q9NSK4; Q9NUS8;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
GN Muskelein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain, Kidney, Lung, and Osteosarcoma;
RX MEDLINE=20108780; PubMed=10640805;
RA Adams J.C., Zhang L.;
RT "cDNA cloning of human muskelein and localisation of the muskelein
RT (MKLN) gene to human chromosome 7q32 and mouse chromosome 6 B1/B2 by
RT physical mapping and FISH.";
RL Cytogenet. Cell Genet. 87:19-21(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Ishihashi T., Fujimori K.,
RA Tanai H., Kimata M., Watanabe M., Hiraoka S., Ishii S., Kawai Y.,
RA Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahara K.,
RA Masuko Y., Kanehori K.;
RT "NEO human cDNA sequencing project.";
RT Submitted (FEB-2000) to the EMBL/Genbank/DBJ databases.
RN [3]
RP SEQUENCE OF 186-735 FROM N.A.
RC TISSUE=Uterus;
RX MEDLINE=22388257; PubMed=12477932;
RA Strassburg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
RA Altshuler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton L., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carinci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunatratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huliy S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.M., Touchman J.W., Green E.D., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";


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RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RN SEQUENCE OF 320-735 FROM N.A.
RC TISSUE=Melanoma;
RC Bloembergen H., Boecher M., Brandt P., Mewes H.-W., Weill B., Wiemann S.;
RU Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Acts as a mediator of cell spreading and cytoskeletal
CC responses to the extracellular matrix component thrombospondin 1
CC (By similarity).
CC -1- SUBUNIT: Binds with the C-terminal tail of the prostaglandin EP3
CC receptor alpha isoform (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Contains 5 Kelch repeats.
CC -1- SIMILARITY: Contains 1 Lish domain.
CC -1- SIMILARITY: Contains 1 CTUH domain.
CC -1- CAUTION: Ref.2 sequence differs from that shown due to a
CC stop codon in position 171.
CC -----
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CC -----
DR EMBL: AF047489; AAF06698.1; ALT SEQ.
DR EMBL: AK002024; BAA92042.1; ALT INIT.
DR EMBL: BC002834; AAH02834.1; ALT INIT.
DR EMBL: AL152071; CAB82407.1;
DR PIR: T47173; T47173.
DR MIM: 605623;
DR Genew: HGNC:7109; MKLN1.
DR InterPro: IPR006595; CTUH.
DR InterPro: IPR006552; Kelch_rep.
DR InterPro: IPR005594; Lish.
DR Pfam: PF01344; Kelch; 3.
DR SMART: SM00668; CTUH; 1.
DR SMART: SM00667; Lish; 1.
DR PROSITE: PS50897; CTUH; 1.
DR PROSITE: PS50896; Lish; 1.
KM Kelch repeat; Repeat.
FT DOMAIN 172 204 LISH.
FT REPEAT 206 258 CTUH.
FT REPEAT 284 330 KELCH 1.
FT REPEAT 339 351 KELCH 2.
FT REPEAT 358 368 KELCH 3.
FT REPEAT 369 379 KELCH 4.
FT REPEAT 380 390 KELCH 5.
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FT REPEAT 526 578 KELCH 5.
 SQ SEQUENCE 735 AA; 84877 MM; 780C8D2CB8C242AA CRC64;
 Query Match 31.2%; Score 35; DB 1; Length 735;
 Best Local Similarity 63.6%; Pred. No. 75;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 11 SKOXBEEAVRL 21
 DB 169 SKYRGEAIRL 179

RESULT 24
 ID MKLN RAT STANDARD; PRT; 735 AA.
 AC 099EV3;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Muskelein.
 GN MKLN1 OR MSG.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_Taxid=10116;
 [1]
 RP SEQUENCE FROM N.A. AND INTERACTION WITH EP3-ALPHA.
 RX MEDLINE=20462961; PubMed=11006128;
 RA Hasegawa H., Katch H., Fujita H., Mori K., Negishi M.;
 RT "Receptor isoform-specific interaction of prostaglandin EP3 receptor with muskelein."
 RL Biochem. Biophys. Res. Commun. 276:350-354(2000).
 CC -1- FUNCTION: Acts as a mediator of cell spreading and cytoskeletal responses to the extracellular matrix component thrombospondin 1 (By similarity).
 CC -1- SUBUNIT: Binds with the C-terminal tail of the prostaglandin EP3 receptor alpha isoform.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: Contains 5 Kelch repeats.
 CC -1- SIMILARITY: Contains 1 Lish domain.
 CC -1- SIMILARITY: Contains 1 CTLD domain.
 CC
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 CC
 CC EMBL; AB046442; BA521439.1; -
 DR InterPro; IPR006595; CTLD.
 DR InterPro; IPR006594; Kelch_rep.
 DR InterPro; IPR006594; Lish.
 DR Pfam; PF01344; Kelch; 3.
 DR SMART; SM00668; CTLD; 1.
 DR SMART; SM00667; Lish; 1.
 DR PROSITE; PSS0897; CTLD; 1.
 DR PROSITE; PSS0896; Lish; 1.
 DR Kelch repeat; Repeat.
 KM
 FT DOMAIN 172 204 LISH.
 FT DOMAIN 206 258 CTLD.
 FT REPEAT 284 330 KELCH 1.
 FT REPEAT 339 391 KELCH 2.
 FT REPEAT 400 458 KELCH 3.
 FT REPEAT 469 515 KELCH 4.
 FT REPEAT 526 578 KELCH 5.
 SQ SEQUENCE 735 AA; 84833 MM; 79BD0B8F74419E76 CRC64;
 Query Match 31.2%; Score 35; DB 1; Length 735;
 Best Local Similarity 63.6%; Pred. No. 75;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 11 SKOXBEEAVRL 21
 DB 169 SKYRGEAIRL 179

RESULT 25
 ID LMG2 MOUSE STANDARD; PRT; 1191 AA.
 AC 061052;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Laminin gamma-2 chain precursor (Laminin/nicein/epiligrin 100 kDa subunit) (Laminin B2c chain).
 GN LAMC2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB; TISSUE=Lung;
 RX MEDLINE=95188894; PubMed=7882992;
 RA Sugiyama S., Uchii A., Yamada S., Kozak C.A., Yamada Y.;
 RT "Cloning and expression of the mouse laminin gamma 2 (B2c) chain, a subunit of epithelial cell laminin."
 RL Eur. J. Biochem. 228:120-128(1995).
 [2]
 RP REVISIONS.
 RA Sasaki T., Yamada Y.;
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 RN (3)
 RP BINDING TO HEPARIN, FIBULIN AND NIDDOGEN, AND MUTAGENESIS OF ARG-76;
 RP ARG-78; PHE-202; LYS-206; CYS-442 AND CYS-445.
 RC STRAIN=FVB; TISSUE=Lung;
 RX MEDLINE=21592560; PubMed=11733994;
 RA Sasaki T., Goehring W., Mann K., Brakebusch C., Yamada Y.,
 RA Faessler R., Timpl R.;
 RT "Short arm region of laminin-5 gamma2 chain: structure, mechanism of processing and binding to heparin and proteins."
 RL J. Mol. Biol. 314:751-763(2001).
 CC -1- FUNCTION: Binding to cells via a high affinity receptor, laminin is thought to mediate the attachment, migration, and organization of cells into tissues during embryonic development by interacting with other extracellular matrix components.
 CC -1- SUBUNIT: Laminin is a complex glycoprotein, consisting of three different polypeptide chains (alpha, beta, gamma), which are bound to each other by disulfide bonds into a cross-shaped molecule comprising one long and three short arms with globules at each end. The gamma-2 chain is a subunit of laminin-5 (epiligrin/kalinin/nicein) and binds fibulin-1, fibulin-1c, fibulin-2 and nidogen.
 CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR; FOUND IN THE BASEMENT MEMBRANES (MAJOR COMPONENT).
 CC -1- TISSUE SPECIFICITY: EPITHELIAL CELLS OF MANY TISSUES, PARTICULARLY HIGH LEVELS IN TONGUE, HAIR FOLLICLES AND KIDNEY. BASEMENT MEMBRANES OF THE COLLECTING TUBULES OF KIDNEY AND PANCREAS.
 CC -1- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.
 CC -1- DOMAIN: DOMAIN IV IS GLOBULAR.
 CC -1- MISCELLANEOUS: Binds heparin.
 CC -1- SIMILARITY: Contains 8 laminin IV domain.
 CC -1- SIMILARITY: Contains 1 laminin IV domain.
 CC
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 CC
 CC EMBL; U43327; AAA85256.2; -

DR HSP: P02468; 1TLE.
 DR MGD: MGI:99913; Ianc2
 DR InterPro: IPR006209; EGF like.
 DR InterPro: IPR000034; Laminin_B.
 DR InterPro: IPR002049; Laminin_EGF.
 DR Pfam: PFO0052; laminin_B; 1.
 DR Pfam: PFO0053; laminin_EGF; 5.
 DR PRINTS: PR00011; EGF_LAMININ.
 DR SMART: SM00181; EGF; 7.
 DR SMART: SM00180; EGF_Lam; 7.
 DR SMART: PS00022; EGF-1; 4.
 DR PROSITE: PS01186; EGF-2; 2.
 DR PROSITE: PS01248; LAMININ TYPE EGF; 6.
 DR GlycoProtex: Basement membrane; Extracellular matrix; Coiled coil;
 KW Laminin EGF-like domain; Cell adhesion; Repeat; Signal;
 KM Hepatin-binding.
 FT SIGNA 1 21 POTENTIAL.
 FT CHAIN 22 1191 LAMININ GAMMA-2 CHAIN.
 FT DOMAIN 28 83 LAMININ EGF-LIKE 1.
 FT DOMAIN 84 130 LAMININ EGF-LIKE 2.
 FT DOMAIN 139 186 LAMININ EGF-LIKE 3.
 FT DOMAIN 187 196 LAMININ EGF-LIKE 4 (N-TERMINAL).
 FT DOMAIN 197 381 LAMININ DOMAIN IV.
 FT DOMAIN 382 415 LAMININ EGF-LIKE 4 (C-TERMINAL).
 FT DOMAIN 416 461 LAMININ EGF-LIKE 5.
 FT DOMAIN 462 516 LAMININ EGF-LIKE 6.
 FT DOMAIN 517 572 LAMININ EGF-LIKE 7.
 FT DOMAIN 573 602 LAMININ EGF-LIKE 8 (INCOMPLETE).
 FT DOMAIN 603 1191 DOMAIN II AND I.
 FT DOMAIN 612 710 COILED COIL (POTENTIAL).
 FT DOMAIN 759 786 COILED COIL (POTENTIAL).
 FT DOMAIN 946 996 COILED COIL (POTENTIAL).
 FT DOMAIN 1139 1178 COILED COIL (POTENTIAL).
 FT DOMAIN 1139 588 COILED COIL (POTENTIAL).
 FT SITE 586 588 CELL ATTACHMENT SITE (POTENTIAL).
 FT DISULFID 84 96 BY SIMILARITY.
 FT DISULFID 86 102 BY SIMILARITY.
 FT DISULFID 104 113 BY SIMILARITY.
 FT DISULFID 116 128 BY SIMILARITY.
 FT DISULFID 139 150 BY SIMILARITY.
 FT DISULFID 141 155 BY SIMILARITY.
 FT DISULFID 157 166 BY SIMILARITY.
 FT DISULFID 169 184 BY SIMILARITY.
 FT DISULFID 462 470 BY SIMILARITY.
 FT DISULFID 464 481 BY SIMILARITY.
 FT DISULFID 484 493 BY SIMILARITY.
 FT DISULFID 496 514 BY SIMILARITY.
 FT DISULFID 517 531 BY SIMILARITY.
 FT DISULFID 519 538 BY SIMILARITY.
 FT DISULFID 541 550 BY SIMILARITY.
 FT DISULFID 553 570 BY SIMILARITY.
 FT DISULFID 610 610 INTERCHAIN (PROBABLE).
 FT DISULFID 613 613 INTERCHAIN (WITH BETA-3 CHAIN) (PROBABLE).
 FT DISULFID 1182 1182 INTERCHAIN (WITH BETA-3 CHAIN) (PROBABLE).
 FT CARBOHYD 342 342 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 362 362 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 526 526 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 941 941 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1032 1032 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT MUTAGEN 76 76 R->A: NO CHANGE TO HERRIN-BINDING.
 FT MUTAGEN 78 78 R->A: NO CHANGE TO HERRIN-BINDING.
 FT MUTAGEN 202 202 F->A: NO CHANGE TO HERRIN-BINDING.
 FT MUTAGEN 206 206 FIBULIN-2 BINDING.
 FT MUTAGEN 206 206 K->A: NO FIBULIN-1C BINDING. NO CHANGE TO FIBULIN-2 BINDING.
 FT MUTAGEN 442 442 C->S: 20-FOLD REDUCTION TO FIBULIN-2 BINDING.
 FT MUTAGEN 445 445 C->S: 20-FOLD REDUCTION TO FIBULIN-2 BINDING.
 SQ SEQUENCE 1191 AA; 130160 MW; 7016C1F651D90B9 CRG64;

Query Match 31.2%; Score 35; DB 1; Length 1191;
 Best Local Similarity 29.2%; Pred. No. 1.2e+02;

Matches 7; Conservative 6; Mismatches 11; Indels 0; Gaps 0;
 QY 11 SKXEEBVRXXXXXGXSGA 34
 DB 784 TEDYSKQALSLARKLLSGGSGS 807
 RESULT 26
 ID MYO6 HUMAN STANDARD; PRT; 1262 AA.
 AC Q9UM54;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Myosin VI.
 GN MYO6.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A. PubMed=9259267;
 RX MEDLINE=97402203; Avraham K.B., Hasson T., Sobe T., Balsara B., Teesla J.R.,
 RA Skvorak A.B., Morton C.C., Copeland N.G., Jenkins N.A.,
 RT "Characterization of unconventional MYO6, the human homologue of the
 RT gene responsible for deafness in Snell's waltzer mice."
 RL Hum. Mol. Genet. 6:1225-1231(1997).
 RN [2]
 RP REVISIONS.
 RA Avraham K.B.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 RP [3]
 RP FUNCTION.
 RX MEDLINE=99447046; PubMed=10519557;
 RA Wells A.L., Lin A.W., Chen L.-Q., Saffer D., Cain S.M., Hasson T.,
 RA Carragher B.O., Milligan R.A., Sweeney H.L.;
 RL "Myosin VI is an actin-based motor that moves backwards."
 RL Nature 401:505-508(1999).
 RN [4]
 RP VARIANT DFN22 TYR-442.
 RX MEDLINE=21375673; PubMed=11466889;
 RA Melchionda S., Ahlert N., Bisceglia L., Sobe T., Glaser F.,
 RA Radonnet R., Arbones M.L., Notarangelo A., Di Iorio E., Carolla M.,
 RA Zelante L., Battivelli X., Avraham K.B., Gasparini P.;
 RT "MYO6, the human homologue of the gene responsible for deafness in
 RT Snell's waltzer mice, is mutated in autosomal dominant nonsyndromic
 RT hearing loss."
 RL Am. J. Hum. Genet. 69:635-640(2001).
 CC -1- FUNCTION: RECESSIVE ACTIN-BASED MOTOR. REQUIRED FOR STRUCTURAL
 CC INTEGRITY OF INNER EAR HAIR CELLS (BY SIMILARITY).
 CC -1- DISEASE: Defects in MYO6 are the cause of an autosomal dominant
 CC form of nonsyndromic sensorineural deafness (DFN22). The deafness
 CC is progressive and postlingual, with onset during childhood (8 to
 CC 10 years of age at onset of symptoms; 6 to 8 years of age at onset
 CC of first audiometric abnormalities). By the age of approximately
 CC 50 years, affected individuals invariably have profound
 CC sensorineural deafness.
 CC -1- SIMILARITY: Contains 1 myosin-like globular head domain.
 CC -1- SIMILARITY: Contains 1 IQ domain.
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 CC or send an email to license@isb-sib.ch).
 CC DR EMBL; U90236; AAC51654.2; -
 DR HSP; P08799; IAMD.
 DR Genew; HGNC:7605; MYO6.
 DR MIM; 600970; -

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DR MIM: 506346; C:unconventional myosin; TAS.
DR GO: GO:0016461; C:unconventional myosin; TAS.
DR GO: GO:0003779; F:actin binding activity; TAS.
DR GO: GO:0005524; F:ATP binding activity; NAS.
DR GO: GO:0006307; F:structural constituent of muscle; NAS.
DR GO: GO:0006941; F:striated muscle contraction; NAS.
DR InterPro: IPR000448; IQ region.
DR InterPro: IPR01609; myosin_head.
DR Pfam: PF00612; IQ; 1.
DR Pfam: PF00612; myosin_head; 1.
DR PRINTS: PR00193; MYOSINHEAVY.
DR ProDom: PD000355; myosin_head; 1.
DR SMART: SM00015; IQ; 1.
DR SMART: SM00242; MYSC; 1.
DR PROSITE: PS50096; IQ; FALSE NEG.
DR Myosin: ATP-binding; Calmodulin-binding; Actin-binding;
KW Coiled coil; Disease mutation; Deafness.
FT DOMAIN 1 759 MYOSIN HEAD-LIKE.
FT DOMAIN 814 834 IQ.
FT DOMAIN 848 1030 COILED COIL (POTENTIAL).
FT NP_BIND 151 158 ATP (POTENTIAL).
FT DOMAIN 665 672 ACTIN-BINDING (POTENTIAL).
FT VARIANT 442 442 C -> Y (IN DENA22).
SQ SEQUENCE 1262 AA; 146047 MW; CFIFA35796FC1C60 CRC64;
Query Match 31.2%; Score 35; DB 1; Length 1262;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 12 KQEEEAURL 21
Db 917 KQEEEAURL 926

RESULT 27
MYO6_MOUSE STANDARD; PRT; 1265 AA.
ID MYO6_MOUSE
AC Q64331;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Myosin VI.
GN MYO6 OR SV.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Scurionath; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=96083582; Pubmed=7493015;
RX Avraham K.B., Hasson T., Steel K.P., Kingsley D.M., Russell L.B.,
RA Mosseker M.S., Copeland N.G., Jenkins N.A.;
RT "The mouse Snell's waltzer deafness gene encodes an unconventional
RT myosin required for structural integrity of inner ear hair cells.";
RL Nat. Genet. 11:369-375(1995).
CC -1- FUNCTION: RECESSIVE ACTIN-BASED MOTOR. REQUIRED FOR STRUCTURAL
CC INTERITY OF INNER EAR HAIR CELLS (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED. WITHIN THE COCHLEA,
CC EXPRESSED SPECIFICALLY WITHIN THE SENSORY HAIR CELLS.
CC -1- DISEASE: DEFECTS IN MYO6 ARE THE CAUSE OF SNELL'S WALTZER. A
CC CONDITION CHARACTERIZED BY CIRCLING, HEAD-TOSSING, DEAFNESS AND
CC HYPERACTIVITY.
CC -1- SIMILARITY: Contains 1 myosin-like globular head domain.
CC -1- SIMILARITY: Contains 1 IQ domain.
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CC -----
CC EMBL: U49739; AAB00194.1; -.
CC PIR: A59299; A59299.
CC HSSP: P08799; 1MND.
CC MGD: MG1104785; MYO6.
CC InterPro: IPR000046; IQ region.
CC InterPro: IPR01609; myosin_head.
CC Pfam: PF00612; IQ; 1.
CC Pfam: PF00612; myosin_head; 4.
CC PRINTS: PR00193; MYOSINHEAVY.
CC ProDom: PD000355; myosin_head; 1.
CC SMART: SM00015; IQ; 1.
CC SMART: SM00242; MYSC; 1.
CC PROSITE: PS50096; IQ; FALSE NEG.
DR Myosin: ATP-binding; Calmodulin-binding; Actin-binding;
KW Coiled coil; Disease mutation; Deafness.
FT DOMAIN 1 762 MYOSIN HEAD-LIKE.
FT DOMAIN 817 837 IQ.
FT DOMAIN 849 1014 COILED COIL (POTENTIAL).
FT NP_BIND 151 158 ATP (POTENTIAL).
FT DOMAIN 668 675 ACTIN-BINDING (POTENTIAL).
FT VARIANT 766 1265 MISSING (IN SNELL'S WALTZER).
SQ SEQUENCE 1265 AA; 146408 MW; 4F51ABCT2463148C CRC64;
Query Match 31.2%; Score 35; DB 1; Length 1265;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 12 KQEEEAURL 21
Db 920 KQEEEAURL 929

RESULT 28
YH74_YERPE STANDARD; PRT; 85 AA.
ID YH74_YERPE
AC Q82FE0;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein YP01774/Y2534.
GN YP01774 OR Y2534.
OS Yersinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CO-92 / Bivolar Orientalis;
RX MEDLINE=21470413; Pubmed=11586360;
RX Parkhill J., Wren B.W., Thomson N.R., Tibball R.W., Holden M.T.G.,
RA Prentice M.B., Sebahia M., James K.D., Churcher G., Mungall K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Felwell T., Hamlin N., Holroyd S., Jagsi K., Karlyshev A.V.,
RA Leather S., Meule S., Oyston P.C.F., Quail M., Rutherford K.,
RA Simmonds M., Skellon J., Stevens K., Whitehead S., Barrell B.G.;
RT "Genome sequence of Yersinia pestis, the causative agent of plague.";
RL Nature 413:523-527(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=KIMS / Bivolar Mediaevalis;
RX MEDLINE=22137863; Pubmed=12142430;
RX Deng W., Burland V., Plunkett G., III, Boutin A., Mayhew G.F., Liss P.,
RA Perna N.T., Rose D.U., Mau B., Zhou S., Schwartz D.C.,
RA Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
RA Staley S.C., McConough K.A., Nilles M.L., Watson J.S., Blattner F.R.,
RA Perry R.D.;
RT "Genome sequence of Yersinia pestis KIM.";
RL J. Bacteriol. 184:4601-4611 (2002).
CC -1- SIMILARITY: BELONGS TO THE UPF0181 FAMILY.
CC -----

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CC -----
CC EMBL: A041150; CAC90592.1; -
CC EMBL: A013856; AAM8690.1; -
CC PIR: A0216; AD0216.
CC HAMAP: MF_00507; -; 1.
CC InterPro: IPR005371; IPR0181.
CC Pfam: PF03701; PF0181; 1.
CC Hypothetical protein: Complete proteome.
CC SEQUENCE 85 AA; 9720 MW; 3EC4ADCA53F29ABE CRC64;

Query Match 30.4%; Score 34; DB 1; Length 85;
Best Local Similarity 34.8%; Pred. No. 12;
Matches 8; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 11 SKQEEAVRLXXXXLXGXSG 33
DB 9 SHEEQEAVRLHKKFSEGMSG 31

RESULT 29
TPIS_MACMU STANDARD; PRT; 248 AA.

AC P15426; 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Triosephosphate isomerase (EC 5.3.1.1) (TIM).
GN TIM.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
NC NCB1_TaxID=9544;
LN [1]
RX MEDLINE=89016592; PubMed=3174447;
RA Old S.E., Mohrenweiser H.W.;
RT "Nucleotide sequence of the triosephosphate isomerase gene from
RT Macaca mulatta".
RL Nucleic Acids Res. 16:9055-9055(1988).
CC -1- CATALYTIC ACTIVITY: D-glyceralddehyde 3-phosphate = glycerone
CC phosphate.
CC -1- PATHWAY: plays an important role in several metabolic pathways.
CC -1- SUBUNIT: Homodimer.
CC -1- SIMILARITY: BELONGS TO THE TRIOSEPHOSPHATE ISOMERASE FAMILY.
CC -----
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CC EMBL: M37572; AAA36922.1; -
CC EMBL: M37561; AAA36922.1; JOINED.
CC EMBL: M37562; AAA36922.1; JOINED.
CC EMBL: M37563; AAA36922.1; JOINED.
CC EMBL: M37564; AAA36922.1; JOINED.
CC EMBL: M37570; AAA36922.1; JOINED.
CC EMBL: M37571; AAA36922.1; JOINED.
CC PIR: S01378; ISMOTR.
CC HSP: P00938; IHTI.
CC InterPro: IPR000652; Triophos_ismrse.
CC Pfam: PF00121; TIM; 1.
CC ProDom: PD001005; Triophos_ismrse; 1.

DR TIGRFAMs: TIGR00419; tim; 1.
DR PROSITE: PS00171; TIM; 1.
KW isomerase; Glycolysis; Gluconeogenesis; Fatty acid biosynthesis;
KW Pentose shunt.
FT INIT MET 0 0 BY SIMILARITY.
FT ACT_SITE 95 95 BY SIMILARITY.
FT ACT_SITE 165 165 BY SIMILARITY.
FT SEQUENCE 248 AA; 26579 MW; 12B170709B9F8FB6 CRC64;

Query Match 30.4%; Score 34; DB 1; Length 248;
Best Local Similarity 24.4%; Pred. No. 37;
Matches 11; Conservative 4; Mismatches 16; Indels 14; Gaps 1;

QY 4 GTXXXXXSKOE-----EAVRLXXXXLXGXSGCA 34
DB 171 GTGKTATPQQAQVYHETKRLGKLSNVEAVAGSRRIRIYGSSVGA 215

RESULT 30
ARGC_LEPIN STANDARD; PRT; 338 AA.

AC P59307; 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE N-acetyl-gamma-glutamyl-phosphate reductase (EC 1.2.1.38) (AGPR) (N-
DE acetyl-glutamate semialdehyde dehydrogenase) (NAGSA dehydrogenase).
GN ARGC OR LA2178.
OS Leptospira interrogans.
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
OC NCB1_TaxID=173;
LN [1]
RX MEDLINE=22598143; PubMed=12712204;
RA Ren S.-X., Fu G., Jiang X.-G., Zeng R., Miao Y.-G., Xu H.,
RA Zhang Y.-X., Xiong H., Lu L.-F., Jiang H.-Q., Jia J., Tu Y.-F.,
RA Jiang Y.-X., Gu W.-Y., Zhang Y.-Q., Cai Z., Sheng H.-H., Yin H.-F.,
RA Zhang Y., Zhu G.-F., Wan M., Huang H.-L., Qian Z., Wang S.-Y., Ma W.,
RA Yao Z.-J., Shen Y., Qiang B.-Q., Xia Q.-C., Guo X.-K., Danchin A.,
RA Saint Girons I., Somerville R.L., Wen Y.-M., Shi W.-H., Chen Z.,
RA Xu J.-G., Zhao G.-P.;
RT "unique physiological and pathogenic features of Leptospira
RT interrogans revealed by whole-genome sequencing";
RL Nature 422:888-893(2003).
CC -1- CATALYTIC ACTIVITY: N-acetyl-L-glutamate 5-semialdehyde + NADPH(+)
CC + phosphate = N-acetyl-5-glutamyl phosphate + NADPH.
CC -1- PATHWAY: Arginine biosynthesis; third step.
CC -1- SIMILARITY: Belongs to the NAGSA dehydrogenase family. Subfamily
CC 1.

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CC EMBL: A011388; AAM49377.1; -
CC HAMAP: MF_00150; -; 1.
CC Pfam: PF01118; Semialdehyde_dh; 1.
CC Pfam: PF02774; Semialdehyde_dhc; 1.
CC ProDom: PD003765; AGPR_act_site; 1.
CC PROSITE: PS01224; ARGC; FALSE NEG.
CC Arginine biosynthesis; Oxidoreductase; NADP; Complete proteome.
CC ACT_SITE 148 148 BY SIMILARITY.
CC SEQUENCE 338 AA; 37839 MW; 70517B5A85BD44 CRC64;

Query Match 30.4%; Score 34; DB 1; Length 338;
Best Local Similarity 38.9%; Pred. No. 51;
Matches 7; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

Mon Dec 29 06:32:10 2003

us-09-889-331a-48.rsp

Page 19

Qy 11 SKOXEEAVRLXXXXLXG 28
Db 22 SRQKEHEVVHITSDKLAG 39

Search completed: December 23, 2003, 10:01:59
Job time : 11 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 23, 2003, 09:59:56 ; Search time 28.5 Seconds
(without alignments)
362.179 Million cell updates/sec

Title: US-09-889-331A-48
Perfect score: 112
Sequence: 1 XXXGTXXXXXSKQEEEAVALRLLXXXXLXGXSXGAXXXXXX 40

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 50 summaries

Database :
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rhodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteria:*
17: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	36.6	324	2	Q8G53 Hellobacill
2	40.5	36.2	458	10	Q49922 Physcomit
3	40.5	36.2	464	10	Q9145 Physcomit
4	40	35.7	347	17	Q9744 Thermoplas
5	39	34.8	189	16	Q8UB5 Agrobacteri
6	39	34.8	193	16	Q98F31 Agrobacteri
7	39	34.8	369	16	Q9RD53 Agrobacteri
8	39	34.8	781	10	Q9C812 Arabidopsis
9	38.5	34.4	468	8	Q95DV5 Nicotiana t
10	38.5	34.4	468	10	Q9M436 Nicotiana t
11	38	33.9	163	11	Q9JLY9 Mus musculu
12	38	33.9	208	17	Q58594 Pyrococcus
13	38	33.9	289	11	Q70379 Mus musculu
14	38	33.9	310	2	Q8LIM2 Escherichia
15	38	33.9	310	2	Q8XCN1 Escherichia
16	38	33.9	310	16	Q8IFG1 Escherichia

17	38	33.9	313	15	Q8ZNA4 Salmonella
18	38	33.9	313	16	Q8ZAY7 Salmonella
19	38	33.9	317	10	Q94D21 Oryza sativa
20	38	33.9	424	4	Q9HD72 Homo sapien
21	38	33.9	426	2	Q8KLD9 Homo sapien
22	38	33.9	537	4	Q9HBE3 Homo sapien
23	38	33.9	537	4	Q9HBE2 Homo sapien
24	38	33.9	537	4	Q9PIA9 Homo sapien
25	38	33.9	616	4	Q9Y529 Homo sapien
26	38	33.9	631	2	Q8RW05 Homo sapien
27	38	33.9	641	2	Q9UDU0 Homo sapien
28	38	33.9	641	11	Q9JMG9 Homo sapien
29	38	33.9	687	4	Q9HBE1 Homo sapien
30	37.5	33.5	478	16	Q8XZES Herpes simp
31	37.5	33.5	785	12	P89451 Brucella su
32	37.5	33.5	191	16	Q8FYU2 Brucella me
33	37	33.0	207	16	Q8YU08 Homo sapien
34	37	33.0	246	4	Q9H6G1 Homo sapien
35	37	33.0	264	4	Q96H23 Homo sapien
36	37	33.0	328	10	Q50007 Homo sapien
37	37	33.0	355	17	Q980M3 Homo sapien
38	37	33.0	393	4	Q96SD6 Homo sapien
39	37	33.0	470	4	Q9NV05 Homo sapien
40	37	33.0	470	4	Q96TC7 Homo sapien
41	37	33.0	492	16	Q9F3D1 Homo sapien
42	37	33.0	524	11	Q9R027 Homo sapien
43	37	33.0	658	17	Q8PYJ7 Homo sapien
44	37	33.0	850	5	Q9WSM8 Homo sapien
45	37	33.0	850	5	Q24211 Homo sapien
46	37	33.0	880	12	Q9DWB5 Homo sapien
47	37	33.0	1041	16	Q981Z6 Homo sapien
48	36.5	32.6	124	16	Q9X8X6 Homo sapien
49	36.5	32.6	456	3	Q06821 Homo sapien
50	36	32.1	83	11	P81799 Rattus norv

ALIGNMENTS

RESULT 1

Q8G53 PRELIMINARY: PRT: 324 AA.

AC Q8G53; 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Aspartate carboxyltransferase (EC 2.1.3.2) (Fragment).
OS Hellobacillus mobilis.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Hellobacteriaceae;
OC Hellobacillus.
OX NCBI_Taxid=28064;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=22337798; PubMed=12446909;
RA Raymond J., Zhaxybayeva O., Gogarten J.P., Gerdes S.Y.,
RT "Whole-genome analysis of photosynthetic prokaryotes.";
RL Science 298:1616-1620(2002).

RP SEQUENCE FROM N.A.
RA Liolios K.G., Chu L., Ostrovskaya O., Mendysheva N., Koukharanko V.,
RA Gerdes S., Kyriades N., Overbeek R.;
RL Submitted (Aug-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY142765; AAN87369.1; -

KW Transferase. 324
FT NON_TER 324
SQ SEQUENCE 324 AA; 35294 MW; 18993D4AB336CD37 CRC64;

Query Match 36.6%; Score 41; DB 2; Length 324;
Best Local Similarity 56.2%; Pred. No. 9.8;
Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 18 AVRLXXXXLXGXSXG 33

DB 306 AYRMALILYMGCTSSG 321

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RESULT 2
ID 049922 PRELIMINARY; PRT; 458 AA.
AC 049922;
DT 01-JUN-1998 (T-EMBLrel. 06, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (T-EMBLrel. 22, Last annotation update)
DE Plastid division protein ftsz1.
GN FTSZ.
OS Physcomitrella patens (Moss).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
OC Bryopsida; Funariidae; Funariaceae; Physcomitrella.
OX NCBI_TaxID=3218;
RN [1]
RP SEQUENCE FROM N.A.
RA Reski R.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98208546; PubMed=9539743;
RA Strepp R., Scholz S., Kruse S., Speith V., Reski R.;
RT "Plant nuclear gene knockout reveals a role in plastid division of the
RT bacterial cell division protein FtsZ, an ancestral tubulin."
RL Proc. Natl. Acad. Sci. U.S.A. 95:4368-4373(1998).
RN [3]
RP SEQUENCE FROM N.A.
RA Reski R.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Kruse S., Klessling J., Harter K., Rensing S., Decker E., Reski R.;
RT "Two distinct nuclear-encoded plant ftsz-genes are highly conserved,
RT both their encoded proteins are imported into chloroplasts and both are
RT indispensable for plastid division."
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ249138; CAB54558.1; -
DR EMBL; AJ249139; CAB54558.1; -
DR HSSP; Q57816; FTSZ.
DR InterPro; IPR000158; FtsZ.
DR InterPro; IPR003008; Tubulin_FtsZ.
DR Pfam; PF00091; tubulin_1.
DR Pfam; PF03953; tubulin_C_1.
DR PRINTS; PR00423; CELLDVIFTSZ.
DR TIGRFAMs; TIGR00065; ftsz_1.
DR PROSITE; PS0135; FTSZ_2; 1.
DR GTP-binding; Transic peptide.
KW TRANSIT.
FT CHAIN 32 458
FT SEQUENCE 458 AA; 47536 MW; 85FB987BCB09B4F CRC64;
QY 4 GTXXXXXSKXKEEAVR-----LXXXXLXGXSSGA 34
DB 169 GCSAAEESKAMVEALRGADWVFTAGMGGTGSQA 204
Query Match 36.2%; Score 40.5; DB 10; Length 458;
Best Local Similarity 33.3%; Pred. No. 18;
Matches 12; Conservative 2; Mismatches 17; Indels 5; Gaps 1;
RESULT 3
ID 09LDK5 PRELIMINARY; PRT; 464 AA.
AC 09LDK5;
DT 01-OCT-2000 (T-EMBLrel. 15, Created)
DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Plastid division protein ftsz2 precursor.
GN FTSZ.
OS Physcomitrella patens (Moss).

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OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
OC Bryopsida; Funariidae; Funariaceae; Physcomitrella.
OX NCBI_TaxID=3218;
RN [1]
RP SEQUENCE FROM N.A.
RA Kruse S., Klessling J., Harter K., Rensing S., Decker E., Reski R.;
RT "Two distinct nuclear-encoded plant ftsz-genes are highly conserved,
RT both their encoded proteins are imported into chloroplasts and both are
RT indispensable for plastid division."
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ249140; CAB56387.1; -
DR EMBL; AJ249139; CAB76386.1; -
DR HSSP; Q57816; FTSZ.
DR InterPro; IPR000158; FtsZ.
DR InterPro; IPR000217; Tubulin.
DR InterPro; IPR003008; Tubulin_FtsZ.
DR Pfam; PF00091; tubulin_1.
DR Pfam; PF03953; tubulin_C_1.
DR PRINTS; PR00423; CELLDVIFTSZ.
DR TIGRFAMs; TIGR00065; ftsz_1.
DR PROSITE; PS0135; FTSZ_2; 1.
DR PROSITE; PS00227; TUBULIN; 1.
DR GTP-binding; Transic peptide.
KW TRANSIT.
FT CHAIN 40 464
FT SEQUENCE 464 AA; 48423 MW; 8D659C5D2DEC0D3 CRC64;
QY 4 GTXXXXXSKXKEEAVR-----LXXXXLXGXSSGA 34
DB 177 GCSAAEESKAMVEALRGADWVFTAGMGGTGSQA 212
Query Match 36.2%; Score 40.5; DB 10; Length 464;
Best Local Similarity 33.3%; Pred. No. 18;
Matches 12; Conservative 2; Mismatches 17; Indels 5; Gaps 1;
RESULT 4
ID 097AK4 PRELIMINARY; PRT; 347 AA.
AC 097AK4;
DT 01-OCT-2001 (T-EMBLrel. 18, Created)
DT 01-OCT-2001 (T-EMBLrel. 18, Last sequence update)
DT 01-OCT-2002 (T-EMBLrel. 22, Last annotation update)
DE Cell division protein.
GN TW0806 OR TWG0806423.
OS Thermoplasma volcanium.
OC Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;
OC Thermoplasmataceae; Thermoplasmata.
OX NCBI_TaxID=50339;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=GSSI / DSM 4299 / JCM 9571;
RX MEDLINE=20570466; PubMed=11121031;
RA Kawashima T., Amano N., Koike H., Makino S.-I., Higuchi S.,
RA Kawashima-Onya Y., Watanabe K., Yamazaki M., Kanehori K., Kawamoto T.,
RA Nunoshita T., Yamamoto Y., Aramaki H., Makino K., Suzuki M.;
RT "Archaeal adaptation to higher temperatures revealed by genomic
RT sequence of Thermoplasma volcanium."
RL Proc. Natl. Acad. Sci. U.S.A. 97:14257-14262(2000).
DR EMBL; AP000993; BAB59948.1; -
DR InterPro; IPR000158; FtsZ.
DR InterPro; IPR003008; Tubulin_FtsZ.
DR Pfam; PF00091; tubulin_1.
DR Pfam; PF03953; tubulin_C_1.
DR PRINTS; PR00423; CELLDVIFTSZ.
DR TIGRFAMs; TIGR00065; ftsz_1.
KW Complete proteome.
FT SEQUENCE 347 AA; 37421 MW; 5CC382D1BFA82331 CRC64;
QY 8 GTXXXXXSKXKEEAVR-----LXXXXLXGXSSGA 34
DB 177 GCSAAEESKAMVEALRGADWVFTAGMGGTGSQA 212
Query Match 35.7%; Score 40; DB 17; Length 347;
Best Local Similarity 34.8%; Pred. No. 17;
Matches 8; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

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QY 12 KOXEEAVRLXXXLXGXSXSGA 34
 DB 108 KOIDERTIVITAGCGGTGTGA 130

RESULT 5
 ID Q8UBT5 PRELIMINARY; PRT; 189 AA.
 AC Q8UBT5;
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE Transcriptional regulator, Card family.
 GN ATU2965 OR AGR C 5013.
 OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Rhizobiaceae; Rhizobium.
 NCBI_TaxID=176299;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=21608550; PubMed=11743193;
 RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
 RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.P., Jr., Woo L.,
 RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Boye D., Sr.,
 RA Chapman P., Clendenning U., Decherage G., Gillet M., Grant C.,
 RA Kutayavin T., Levy R., Li M.-J., McClelland E., Palmeri A.,
 RA Raymond C., Rouse G., Saenphimachak C., Wu Z., Romero P., Gordon D.,
 RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
 RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
 RA Chumley P., Tingley S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
 RA Nester E.W.,
 RT "The genome of the natural genetic engineer Agrobacterium tumefaciens C58."
 RL Science 294:2317-2323(2001).
 RN [2]

RP SEQUENCE FROM N.A.
 RX MEDLINE=21608551; PubMed=11743194;
 RA Goodner E., Hinkle G., Gattling S., Miller N., Blanchard M.,
 RA Qurollo B., Goldman B.S., Cao Y., Akenazi M., Halling L.,
 RA Houmlet K., Gordon J., Vandin M., Iatchouk O., Egg A., Liu F.,
 RA Wollam C., Allinger M., Doughly D., Scott C., Lappas C., Markelz B.,
 RA Flanagan C., Crowell C., Giron J., Lomo C., Sear C., Strub G.,
 RA Cielo C., Slater S.,
 RT "Genome sequence of the plant pathogen and biotechnology agent Agrobacterium tumefaciens C58."
 RL Science 294:2323-2328(2001).
 RX EMBL; AE009224; AAL43746.1;
 DR EMBL; AE008190; AAK8480.1;
 DR InterPro; IPR003711; CARD.
 DR Pfam; PF02559; TP_Card; 1.
 KW Complete proteome.
 RN [3]

RP SEQUENCE FROM N.A.; 21150 MW; 765DAF2MA10A3DC4 CRC64;
 SO

Query Match 34.8%; Score 39; DB 16; Length 189;
 Best Local Similarity 43.5%; Pred. No. 14;
 Matches 10; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

QY 11 SKOXEEAVRLXXXLXGXSXSG 33
 DB 154 NKMSFEAVRLVNLAKPKRG 176

RESULT 6
 ID Q98FB1 PRELIMINARY; PRT; 193 AA.
 AC Q98FB1;
 DT 01-OCT-2001 (TREMBlrel. 18, Created)
 DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
 DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)
 DE Transcriptional factor regulator.
 GN MLR3857.
 OS Rhizobium loti (Mesorhizobium loti).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;

OC Phyllobacteriaceae; Mesorhizobium.
 OX NCBI_TaxID=381;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=MAFF303099;
 RC MEDLINE=21082930; PubMed=11214968;
 RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
 RA Matanabe A., Idehara K., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
 RA Mochizuki Y., Nakayama S., Nakazaki N., Shimo S., Sugimoto M.,
 RA Takeuchi C., Yamada M., Tabata S.,
 RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium Mesorhizobium loti."
 RL DNA Res. 7:331-338(2000).
 RX EMBL; AP003002; BAB50656.1;
 DR InterPro; IPR003711; CARD.
 DR Pfam; PF02559; TP_Card; 1.
 KW Complete proteome.
 RN [4]

RP SEQUENCE FROM N.A.; 21811 MW; 53B7FPCSE907B538 CRC64;
 SO

Query Match 34.8%; Score 39; DB 16; Length 193;
 Best Local Similarity 41.7%; Pred. No. 14;
 Matches 10; Conservative 2; Mismatches 12; Indels 0; Gaps 0;

QY 11 SKOXEEAVRLXXXLXGXSXSGA 34
 DB 157 NKMSFEAVRLVNLAKPKRGA 180

RESULT 7
 ID Q9RD53 PRELIMINARY; PRT; 369 AA.
 AC Q9RD53;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Putative transcriptional regulator.
 GN SC00629 OR SCF56.13C.
 OS Streptomyces coelicolor.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycetaceae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1902;
 RN [1]

RP SEQUENCE FROM N.A.
 RX STRAIN=A3(2);
 RA Murphy L., Harris D.,
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]

RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA Cerdano A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]

RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RX MEDLINE=97000351; PubMed=8843436;
 RA Redendach W., Kleiser H.M., Denepaite D., Eichner A., Cullum J.,
 RA Kinashi H., Hopwood D.A.,
 RT "A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb streptomycetes coelicolor A3(2) chromosome."
 RL Mol. Microbiol. 21:77-96(1996).
 RN [4]

RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2) / M145;
 RX MEDLINE=21996410; PubMed=12000953;
 RA Bentley S.D., Chater K.F., Cerdano D.E., Quail M.A., Kleiser H.,
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Collins M.,
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
 RA Huang C.-H., Kleser T., Larke L., Murphy L., Oliver K., O'Neill S.,
 RA Rabinowitch E., Rajandream M.A., Rutherford K., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 RA Warren T., Wietzorek A., Woodward J., Barrell B.G., Parkhill J.,

RA Hopwood D.A.;
 RT "Complete genome sequence of the model actinomycete Streptomyces
 coelicolor A3(2).";
 RL Nature 417:141-147(2002).
 DR EMBL: AL939106; CAB62758.1; -
 DR HSSP; P03023; 110C
 DR InterPro; IPR000843; HTH_Lact.
 DR InterPro; IPR001993; Mitoch_Carrier.
 DR InterPro; IPR001761; Periplasm/Lact.
 DR Pfam; PF00532; Peripla_BP_1like; 1.
 DR SMART; SMO0354; HTH_Lact1; 1.
 DR PROSITE; PS00215; MITOCH_CARRIER; 1.
 KM Complete proteome.
 SQ SEQUENCE 369 AA; 37741 MW; 519C78FD9A04EE9 CRC64;
 Query Match 34.8%; Score 39; DB 16; Length 369;
 Best Local Similarity 47.1%; Pred. No. 28;
 Matches 8; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 17 EAVRLXXXXLXGXSXSG 33
 DB 334 EAVRLATRIACGPAEG 350

RESULT 8
 ID 09C812 PRELIMINARY; PRT; 781 AA.
 AC 09C812;
 DT 01-JUN-2001 (TRENBLrel. 17, Created)
 DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
 DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
 DE Hypothetical 87.1 kDa protein.
 GN F10C21.7.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eucotsids II; Brassicales; Brassicaceae; Arabidopsids.
 OC NCBI_TaxId=3702;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=21016719; PubMed=1130712;
 RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
 White O., Alonso J., Altieri H., Araujo R., Bowman C.L., Brooks S.Y.,
 Buhrer E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
 Chung M.K., Conn L., Conway A.B., Conway A.R., Greasy T.H., Dewar K.,
 Dunn P., Egu P., Feldblyum T.V., Feng U.-D., Fong B., Fujii C.Y.,
 Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huzar L.,
 Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
 Kim C.U., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
 Langin-Hopfer S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
 Lin X., Liu S.X., Liu Z.A., Lueros J.S., Maiti R., Marziani A.,
 Millischer J., Miranda M., Nguyen M., Nietman W.C., Osborne B.I.,
 Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
 Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
 Sun H., Taiton L.J., Tambunga G., Toriumi M.J., Town C.D.,
 Utterback T., Van Aken S., Vayberg M., Vysotskaia V.S., Walker M.,
 Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
 RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
 thaliana.";
 RL Nature 408:816-820(2000).
 DR EMBL; AC051630; AKG51222.1; -
 DR InterPro; IPR002088; PFTA.
 DR InterPro; IPR001214; SET.
 DR InterPro; IPR001440; TPR.
 DR Pfam; PF00515; TPR; 4.
 DR SMART; SMO0028; TPR; 3.
 DR PROSITE; PS00364; PFTA; 1.
 DR PROSITE; PS0280; SET; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 781 AA; 87145 MW; F27B02CA82C35C76 CRC64;
 Query Match 34.8%; Score 39; DB 10; Length 781;

Best Local Similarity 50.0%; Pred. No. 65;
 Matches 9; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 17 EAVRLXXXXLXGXSXSG 34
 DB 722 EAVRLASIGLASGSSGA 739

RESULT 9
 ID 09SDV5 PRELIMINARY; PRT; 468 AA.
 AC 09SDV5;
 DT 01-DEC-2001 (TRENBLrel. 19, Created)
 DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
 DE FtsZ-like protein.
 GN FTSZ.
 OS Nicotiana tabacum (Common tobacco).
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; Lamiales; Solanales; Solanaceae; Nicotiana.
 OC NCBI_TaxId=4097;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Bright Yellow 2;
 RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
 RN (2)
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Bright Yellow 2;
 RA El-Shami M.;
 RL Thesis (2000), Department of Biological Sciences,
 University of Grenoble, Grenoble, France.
 DR EMBL; AJ311847; CAC44257.1; -
 DR InterPro; IPR00158; FtsZ.
 DR InterPro; IPR003008; Tubulin_FtsZ.
 DR Pfam; PF00091; tubulin; 1.
 DR Pfam; PF03953; tubulin_C; 1.
 DR PRINTS; PR00423; CELDVISFTSZ.
 DR TIGRFAMs; TIGR00065; ftsz; 1.
 DR PROSITE; PS01135; FtsZ_2; 1.
 DR GTP-binding; Chloroplast.
 KW GTP-binding; Chloroplast.
 SQ SEQUENCE 468 AA; 49174 MW; 8237DF472D92257F CRC64;
 Query Match 34.4%; Score 38.5; DB 8; Length 468;
 Best Local Similarity 33.3%; Pred. No. 47;
 Matches 12; Conservative 2; Mismatches 17; Indels 5; Gaps 1;

QY 4 GTXXXXXKXKEEVR-----LXXXXLXGXSXSG 34
 DB 176 GMAANESKQATIEAVYGADVFVTMGGGGTGTGA 211

RESULT 10
 ID 09M436 PRELIMINARY; PRT; 468 AA.
 AC 09M436;
 DT 01-OCT-2000 (TRENBLrel. 15, Created)
 DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
 DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
 DE Chloroplast FtsZ-like protein.
 GN FTSZ.
 OS Nicotiana tabacum (Common tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; Lamiales; Solanales; Solanaceae; Nicotiana.
 OC NCBI_TaxId=4097;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA El-Shami M., Alcaraz J.P., Larbs-Mache S., Falconet D.;
 RT "A new cDNA encoding FtsZ-like protein from Nicotiana tabacum.";
 RL Submitted (FEB-2000) to the EMBL/Genbank/DBJ databases.

DR EMBL: AJ271750; CAB89288.1; -
 DR HSSP: O57816; 1FSZ.
 DR InterPro: IPR00158; FtsZ.
 DR InterPro: IPR003008; Tubulin_FtsZ.
 DR Pfam: PF00091; tubulin; 1.
 DR Pfam: PF03953; tubulin_C1.
 DR PRINTS: PR00423; CELDIVISFISZ.
 DR TIGRAME: TIGR00065; ftsz; 1.
 DR PROSITE: PS01135; FTSZ_2; 1.
 KW GTP-binding.
 SQ SEQUENCE 468 AA; 49274 MW; C216D6B2DE167ED3 CRC64;

Query Match 34.4%; Score 38.5; DB 10; Length 468;
 Best Local Similarity 33.3%; Pred. No. 47;
 Matches 12; Conservative 2; Mismatches 17; Indels 5; Gaps 1;

QY 4 GTXXXXXKQXEEAVR-----LXXXXLXGXSXG 34
 DB 176 GMAANESKQALEAVYAGADMFVYAGMGCGTGTGA 211

RESULT 11
 Q9LY9 PRELIMINARY; PRT; 163 AA.
 ID Q9LY9:
 DT 01-OCT-2000 (TRENBLrel. 15, Created)
 DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
 DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
 DE PATZ (Fragment).
 GN ZFP278 OR PATZ.
 OS Mus musculus (mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_TaxID=10090;
 RX MEDLINE=20179892; PubMed=10713105;
 RC STRAIN=C57;
 RA Voliono E., Day P.M., Santoro M., Lanta L., Bruni C.B., Fusco A.,
 RA Chiariotti L.,
 RT "A novel member of the B/B/POZ family, PATZ, associates with the RNP4
 RT RING finger protein and acts as a transcriptional repressor."
 RL J. Biol. Chem. 275:7894-7901 (2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57;
 RA Chiariotti L., Fedele M.;
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF19255; AAF32517.1; -
 DR MGD; MGI:1891832; Zfp278.
 DR InterPro: IPR000637; AT hook.
 DR InterPro: IPR007087; Znf_C2H2.
 DR Pfam: PF02178; AT hook; 1.
 DR Pfam: PF00096; zfc_C2H2; 1.
 DR SMART; SM00384; AT hook; 1.
 DR SMART; SM00355; Znf_C2H2; 1.
 DR PROSITE; PS00354; HMG1_Y; 1.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 1.
 DR PROSITE; PS00157; ZINC_FINGER_C2H2_2; 1.
 KW Metal-binding; Zinc; Zinc-finger.
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 163 AA; 17227 MW; 60A3046938B4FC9D CRC64;

Query Match 33.9%; Score 38; DB 11; Length 163;
 Best Local Similarity 42.9%; Pred. No. 18;
 Matches 9; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 11 SKQEEAVRLXXXXLXGXSXG 31
 DB 2 SMQPEEAPARATGAAIAGGAS 22

RESULT 12
 ID O58594 PRELIMINARY; PRT; 208 AA.
 AC O58594:
 DT 01-AUG-1998 (TRENBLrel. 07, Created)
 DT 01-AUG-1998 (TRENBLrel. 07, Last sequence update)
 DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
 DE 208AA long hypothetical transcription initiation factor IIB.
 GN PH0864.
 OS Pyrococcus horikoshii.
 OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
 OC Pyrococcus.
 ON NCBI_TaxID=53953;
 RX MEDLINE=98344137; PubMed=9679194;
 RA Kawarabayashi Y., Sawada M., Horikawa H., Halkawa Y., Hino Y.,
 RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
 RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
 RA Funahashi T., Tanaka T., Kudoh Y., Yamazaki U., Kushida N., Oguchi A.,
 RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
 RA Maechi Y., Shizuya H., Kikuchi H.;
 RT "Complete sequence and gene organization of the genome of a hyper-
 RT thermophilic archaeobacterium, Pyrococcus horikoshii OT3."
 RL DNA Res. 5:55-76(1998).
 DR EMBL: AP000003; BAA29958.1; -
 DR HSSP; P29095; IAI5.
 DR InterPro: IPR006670; Cyclin.
 DR InterPro: IPR000812; FFIIB_euk.
 DR Pfam: PF00382; transcript_fac2; 2.
 DR PRINTS: PR00685; TIFACTORIIB.
 DR SMART; SM00385; CYCLIN; 2.
 DR PROSITE; PS00782; FFIIB; 1.
 KW Initiation factor; Complete proteome.
 SQ SEQUENCE 208 AA; 23878 MW; CBELA3D30CCT6762 CRC64;

Query Match 33.9%; Score 38; DB 17; Length 208;
 Best Local Similarity 36.4%; Pred. No. 24;
 Matches 8; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

QY 12 KQXEEAVRLXXXXLXGXSXG 33
 DB 38 KXVEREAVRIYKLIKSGVTG 59

RESULT 13
 ID O70379 PRELIMINARY; PRT; 289 AA.
 AC O70379:
 DT 01-AUG-1998 (TRENBLrel. 07, Created)
 DT 01-AUG-1998 (TRENBLrel. 07, Last sequence update)
 DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
 DE Thioresdoxin-related protein.
 GN TXN1.
 OS Mus musculus (mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_TaxID=10090;
 RX MEDLINE=98334653; PubMed=9668102;
 RA Lee K.K., Murakawa M., Takahashi S., Tsubuki S., Kawashima Si.,
 RA Sakamaki K., Yonahara S.;
 RT "Purification, molecular cloning, and characterization of TRP32, a
 RT novel thioresdoxin-related mammalian protein of 32 kDa."
 RL J. Biol. Chem. 273:19160-19166(1998).
 DR EMBL: AF052650; AAC40183.1; -
 DR HSSP; O43396; IGH2.
 DR MGD; MGI:1860078; Txn1.
 DR InterPro: IPR006662; Thiores.
 DR InterPro: IPR006663; Thioresdox_dom2.

DR Pfam: PF00085; Uncloned; 1.
 RA PROSITE: PS00194; THIOREDOXIN; 1.
 SQ SEQUENCE 289 AA; 32251 MW; 0AA39C6C1D1DFD0D CRC64;

Query Match 33.9%; Score 38; DB 11; Length 289;
 Best Local Similarity 44.4%; Pred. No. 34;
 Matches 8; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 11 SKQEEAVRLXXXIXG 28
 DB 250 SKQEEETRIISYFTFG 267

RESULT 14

QBLIM2 PRELIMINARY; PRT; 310 AA.

AC QBLIM2; 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE Putative transporter protein.

GN yfpc.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.

OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=EC3132;

RA Bookman J.;
 RT "Adaption of the sucrose metabolism in the Escherichia coli wild type strain EC3132."

RT Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: X81461; CAD30711.1; -

SQ SEQUENCE 310 AA; 34486 MW; 54AA2C8C6507FEE CRC64;

Query Match 33.9%; Score 38; DB 2; Length 310;
 Best Local Similarity 34.8%; Pred. No. 37;
 Matches 8; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 12 KQEEAVRLXXXIXGSGA 34
 DB 50 KLERDAMALMSAIAAGLSMGA 72

RESULT 15

Q8XCNI PRELIMINARY; PRT; 310 AA.

AC Q8XCNI; 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)

DE Putative transport.
 GN yfpc OR Z3611 OR EC31320.
 OS Escherichia coli O157:H7.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.

OX NCBI_TaxID=83334;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=O157:H7 / EDL933 / ATCC 700927;

RA MEDLINE=21074935; PubMed=11206551;

RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

RA Postel G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,

RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamoustis K.,

RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

RA Welch R.A., Blatner F.R.;
 RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7";
 RL Nature 409:525-533(2001).
 RN [2]
 RP SEQUENCE FROM N.A.

RC STRAIN=O157:H7 / RIMD 0509952;

RX MEDLINE=21156231; PubMed=11258796;
 RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
 RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
 RA Iida T., Takemi H., Honda T., Sasaki K., Ogasawara N., Yasunaga T.,
 RA Kunara S., Shiba T., Hattori M., Shinagawa H.;
 RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
 RT O157:H7 and genomic comparison with a laboratory strain K-12."

RT DNA Res. 8:11-22(2001).
 DR EMBL: AE005466; AAC57475.1; -
 DR EMBL: AP002561; BAB36653.1; -

KM Complete proteome.
 SQ SEQUENCE 310 AA; 34482 MW; 407D21FF665D690 CRC64;

Query Match 33.9%; Score 38; DB 16; Length 310;
 Best Local Similarity 34.8%; Pred. No. 37;
 Matches 8; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 12 KQEEAVRLXXXIXGSGA 34
 DB 50 KLERDAMALMSAIAAGLSMGA 72

RESULT 16

Q8PFG1 PRELIMINARY; PRT; 310 AA.

AC Q8PFG1; 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)

DE Hypothetical protein yfpc.
 GN yfpc OR C2892.

OS Escherichia coli O6.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.

OX NCBI_TaxID=217992;
 RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=O6:H1 / CFT073 / ATCC 700928;

RX MEDLINE=22388234; PubMed=12471157;

RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,

RA Raab D., Buckles E.L., Licu S.-R., Boutin A., Hackett J., Stroud D.,

RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,

RA Mobley H.L.T., Donnenberg M.S., Blatner F.R.;
 RT "Extensive mosaic structure revealed by the complete genome sequence
 RT of uropathogenic Escherichia coli."

RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
 DR EMBL: AE016764; AA081342.1; -

KM Hypothetical protein Complete proteome.
 SQ SEQUENCE 310 AA; 34524 MW; A7AD75C3A31EFBF CRC64;

Query Match 33.9%; Score 38; DB 16; Length 310;
 Best Local Similarity 34.8%; Pred. No. 37;
 Matches 8; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 12 KQEEAVRLXXXIXGSGA 34
 DB 50 KLERDAMALMSAIAAGLSMGA 72

RESULT 17

Q8ZNA4 PRELIMINARY; PRT; 313 AA.

AC Q8ZNA4; 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)

DE Putative transport.

GN yfpc OR STM2393.

OS Salmonella typhimurium.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Salmonella.

OX NCBI_TaxID=602;
 RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porcullik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Milvanev E.,
RA Ryan E., Sun H., Florea L., Miller W., Stenking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
LT2."
RL Nature 413:852-856(2001).
DR EMBL: AE008807; AL21294.1;
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 313 AA; 34917 MW; 430A474E07B640AC CRC64;

Query Match 33.9%; Score 38; DB 16; Length 313;
Best Local Similarity 34.8%; Pred. No. 38;
Matches 8; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 12 KXEEAVRLXXXXLXGXSSGA 34
DB 53 KEMERDAMLLWSAIAAGLSMGA 75

RESULT 18
O824Y7 PRELIMINARY; PRT; 313 AA.
AC O824Y7;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Putative membrane protein.
GN STY2625.
OS Salmonella typhi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OC NCBI_TaxID=601;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Main J.,
RA Churcher C., Mangall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Conerton P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Felwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA Krogan A., Larsen T.S., Leather S., Mould S., O'Gaora P., Parry C.,
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrall B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
enterica serovar Typhi CT18."
RL Nature 413:848-852(2001).
DR EMBL: AL627274; CAD07625.1;
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 313 AA; 34921 MW; EA15DC17146DDDB5 CRC64;

Query Match 33.9%; Score 38; DB 16; Length 313;
Best Local Similarity 34.8%; Pred. No. 38;
Matches 8; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 12 KXEEAVRLXXXXLXGXSSGA 34
DB 53 KEMERDAMLLWSAIAAGLSMGA 75

RESULT 19
O84D21 PRELIMINARY; PRT; 317 AA.
AC O84D21;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE P0025A05.14 protein.

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GN P0025A05.14.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC
clone: P0025A05."
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AP003504; BAB63754.1;
DR Gramene; Q94D21;
SQ SEQUENCE 317 AA; 34212 MW; 2FF23B107514A238 CRC64;

Query Match 33.9%; Score 38; DB 10; Length 317;
Best Local Similarity 40.9%; Pred. No. 38;
Matches 9; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

QY 13 KXEEAVRLXXXXLXGXSSGA 34
DB 163 EANEALALLIDYLSGNSPCA 184

RESULT 20
O9HD72 PRELIMINARY; PRT; 424 AA.
AC O9HD72;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Kruempel-related zinc finger protein SEZFS.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RC Wan T., Li N., Zhang W., Cao X.;
RX Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF242522; AAF99602.1;
DE HSSP; Q05516; ICS3.
DR InterPro: IPR000637; AT hook.
DR InterPro: IPR000210; BTB_POZ.
DR InterPro: IPR007087; Znf_C2H2.
DR Pfam: PF02178; AT_hook.1.
DR Pfam: PF00651; BTB; 1.
DR Pfam: PF00096; zf-C2H2; 3.
DR SMART: SM00384; AT_hook.1.
DR SMART: SM00225; BTB; 1.
DR SMART: SM00355; Znf_C2H2; 3.
DR PROSITE: PS00402; BFD_TRANSF_INN_MEMBER; 1.
DR PROSITE: PS50097; BTB; 1.
DR PROSITE: PS00354; HMGI_Y; 1.
DR PROSITE: PS00028; ZINC_FINGER_C2H2_1; 3.
DR PROSITE: PS50157; ZINC_FINGER_C2H2_2; 3.
KW Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 424 AA; 45257 MW; 6B3CDA886941F20 CRC64;

Query Match 33.9%; Score 38; DB 4; Length 424;
Best Local Similarity 42.9%; Pred. No. 53;
Matches 9; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 11 SKXEEAVRLXXXXLXGXSS 31
DB 205 SMQPEEAAABAAGAAAGAS 225

RESULT 21
O8KLD9

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ID Q8KLD9 PRELIMINARY; PRT; 426 AA.
AC Q8KLD9;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Cytochrome p450, Cyp2.
GN Cyp2.
OS Rhizobium etli.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium.
OC NCBI_TaxID=29449;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CFN42;
RX MEDLINE=9193195; PubMed=2013564;
RA Girard M.L., Flores M., Brom S., Romero D., Palacios R., Davila G.;
RT "Structural complexity of the symbiotic plasmid of Rhizobium
leguminosarum bv. phaseoli.";
RL Bacteriol. 173:2411-2419(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CFN42;
RX MEDLINE=97419521; PubMed=9274036;
RA Ramirez-Romero M.A., Bustos P., Girard L., Rodriguez O.,
Cevallos M.A., Davila G.;
RT "Sequence, localization and characteristics of the replicator region
of the symbiotic plasmid of Rhizobium etli.";
RL Microbiology 143:2825-2831(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=CFN42;
RA Quintero V., Cevallos M.A., Davila G.;
RT "A site-specific recombinase and RecA are required to exert
incompatibility towards the symbiotic plasmid of Rhizobium etli.";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
DR EMBL; U80928; AAMS4801.1;
DR InterPro; IPR001128; Cytochrome_P450.
DR Pfam; PF00067; P450; 1.
DR PRINTS; PS00385; P450.
DR PROSITE; PS00086; CYTOCHROME_P450; 1.
KW Heme, Monooxygenase; Oxidoreductase; Plasmid.
SQ SEQUENCE 426 AA; 46681 MW; 40C9A81F6843347D CRC64;

Query Match 33.9%; Score 38; DB 2; Length 426;
Best Local Similarity 42.9%; Pred. No. 53;
Matches 9; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 12 KQXEEAVRLXXXXLXGXSS 32
DB 220 KATEBAIGLAAGVIVAGHES 240

RESULT 22
Q9HBE3 PRELIMINARY; PRT; 537 AA.
AC Q9HBE3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Zinc finger sarcoma gene short isoform (Zinc finger protein 278).
GN ZSG.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=20404868; PubMed=10949935;
RX MEDLINE=20404868; PubMed=10949935;
RA Mestrangelo T., Modena P., Tornelli S., Bullrich F., Testi A.,
Mezzelani A., Radice P., Azarelli A., Pilotti S., Croce C.,
Pierotti M., Sozzi G.;

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RT "A novel zinc finger gene is fused to EWS in small round cell tumor.";
RL Oncogene 19:3799-3804(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAUSBERG R.;
RA Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF254082; AAG09031.1;
DR EMBL; BC021091; AAH21091.1;
DR HSSP; Q05516; ICS3.
DR InterPro; IPR000637; AT hook.
DR InterPro; IPR000515; BPD_transp.
DR InterPro; IPR000210; BTB_POZ.
DR InterPro; IPR007087; Znf_C2H2.
DR Pfam; PF02178; AT hook; 1.
DR Pfam; PF00651; BTB; 1.
DR Pfam; PF00096; zf_C2H2; 4.
DR ProDom; PD000003; Znf_C2H2; 1.
DR SMART; SM00384; AT hook; 1.
DR SMART; SM00225; BTB; 1.
DR SMART; SM00355; Znf_C2H2; 4.
DR PROSITE; PS00402; BPD_TRANSF_INN_MEMBER; 1.
DR PROSITE; PS00097; BTB; 1.
DR PROSITE; PS00354; HMG1_Y; 1.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 4.
DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 4.
KW Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 537 AA; 57601 MW; BA4A909E24800F13 CRC64;

Query Match 33.9%; Score 38; DB 4; Length 537;
Best Local Similarity 42.9%; Pred. No. 68;
Matches 9; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 11 SKQXEEAVRLXXXXLXGXSS 31
DB 205 SKQXEEAVRLXXXXLXGXSS 225

RESULT 23
Q9HBE2 PRELIMINARY; PRT; 537 AA.
AC Q9HBE2;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Zinc finger sarcoma gene long B isoform.
GN ZSG.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20404868; PubMed=10949935;
RA Mestrangelo T., Modena P., Tornelli S., Bullrich F., Testi A.,
Mezzelani A., Radice P., Azarelli A., Pilotti S., Croce C.,
Pierotti M., Sozzi G.;
RT "A novel zinc finger gene is fused to EWS in small round cell tumor.";
RL Oncogene 19:3799-3804(2000).
DR EMBL; AF254084; AAG09033.1;
DR HSSP; Q05516; ICS3.
DR InterPro; IPR000637; AT hook.
DR InterPro; IPR000515; BPD_transp.
DR InterPro; IPR000210; BTB_POZ.
DR InterPro; IPR007087; Znf_C2H2.
DR Pfam; PF02178; AT hook; 1.
DR Pfam; PF00651; BTB; 1.
DR ProDom; PD000003; Znf_C2H2; 1.
DR SMART; SM00384; AT hook; 1.
DR SMART; SM00225; BTB; 1.
DR SMART; SM00355; Znf_C2H2; 6.
DR PROSITE; PS00402; BPD_TRANSF_INN_MEMBER; 1.

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DR PROSITE; PS00097; BTB; 1.
 DR PROSITE; PS00354; HMG1_Y; 1.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 5.
 DR PROSITE; PS00157; ZINC_FINGER_C2H2_2; 5.
 KW Metal-binding; zinc; zinc-finger
 SQ SEQUENCE 537 AA; 57995 MW; 950792413BF15DB CRC64;

Query Match 33.9%; Score 38; DB 4; Length 537;
 Best Local Similarity 42.9%; Pred. NO. 68;
 Matches 9; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 11 SKQEEAVRLXXXXLXGXS 31
 DB 205 SMQPEEAPARAAGAAIAGQAS 225

RESULT 24
 Q9P1A9 PRELIMINARY; PRT; 537 AA.
 AC Q9P1A9; 01-OCT-2000 (TReMBLrel. 15, Created)
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
 DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
 DE PATZ.
 GN PATZ.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RX SEQUENCE FROM N.A.
 RX MEDLINE=20179892; Pubmed=10713105;
 RA Fedele M., Benvenuto G., Pero R., Majello B., Battista S., Lembo F.,
 RA Volionio E., Day P.M., Santoro M., Lanta L., Bruni C.B., Fusco A.,
 RA Chiacioti L.;
 RA "A novel member of the BTB/POZ family, PATZ, associates with the RNF4
 RT RING finger protein and acts as a transcriptional repressor."
 RT J. Biol. Chem. 275:7894-7901(2000).
 RN [2]

RP SEQUENCE FROM N.A.
 RA Chiacioti L., Fedele M.;
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF119256; AAF32518.1; -.
 DR HSSP; Q05516; ICS3.
 DR InterPro; IPR000637; AT_hook.
 DR InterPro; IPR000515; BPD_transp.
 DR InterPro; IPR000210; BTB_POZ.
 DR InterPro; IPR007087; ZnF_C2H2.
 DR Pfam; PF02178; AT_hook; 1.
 DR Pfam; PF00651; BTB; 1.
 DR Pfam; PF00096; ZF_C2H2; 4.
 DR ProDom; PD000003; ZnF_C2H2; 1.
 DR SMART; SM00384; AT_hook; 1.
 DR SMART; SM00225; BTB; 1.
 DR SMART; SM00355; ZnF_C2H2; 4.
 DR PROSITE; PS00402; BPD_TRANSF_INN_MEMBER; 1.
 DR PROSITE; PS00097; BTB; 1.
 DR PROSITE; PS00354; HMG1_Y; 1.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 4.
 DR PROSITE; PS00157; ZINC_FINGER_C2H2_2; 4.
 KW Metal-binding; zinc; zinc-finger.
 SQ SEQUENCE 537 AA; 57616 MW; 749440224C94750A CRC64;

Query Match 33.9%; Score 38; DB 4; Length 537;
 Best Local Similarity 42.9%; Pred. NO. 68;
 Matches 9; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 11 SKQEEAVRLXXXXLXGXS 31
 DB 205 SMQPEEAPARAAGAAIAGQAS 225

RESULT 25

Q9Y529 PRELIMINARY; PRT; 616 AA.
 ID Q9Y529
 AC Q9Y529;
 DT 01-NOV-1999 (TReMBLrel. 12, Created)
 DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
 DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Collins J.E., Huckle E.J.;
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL096880; CAB51404.1; -.
 DR HSSP; Q05516; ICS3.
 DR InterPro; IPR000637; AT_hook.
 DR InterPro; IPR000515; BPD_transp.
 DR InterPro; IPR000210; BTB_POZ.
 DR InterPro; IPR007087; ZnF_C2H2.
 DR Pfam; PF02178; AT_hook; 1.
 DR Pfam; PF00651; BTB; 1.
 DR Pfam; PF00096; ZF_C2H2; 7.
 DR ProDom; PD000003; ZnF_C2H2; 1.
 DR SMART; SM00384; AT_hook; 1.
 DR SMART; SM00225; BTB; 1.
 DR SMART; SM00355; ZnF_C2H2; 4.
 DR PROSITE; PS00402; BPD_TRANSF_INN_MEMBER; 1.
 DR PROSITE; PS00097; BTB; 1.
 DR PROSITE; PS00354; HMG1_Y; 1.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 6.
 DR PROSITE; PS00157; ZINC_FINGER_C2H2_2; 6.
 KW Hypothetical protein; Metal-binding; zinc; zinc-finger.
 SQ SEQUENCE 616 AA; 66319 MW; EEECEOD1P9288010 CRC64;

Query Match 33.9%; Score 38; DB 4; Length 616;
 Best Local Similarity 42.9%; Pred. NO. 79;
 Matches 9; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 11 SKQEEAVRLXXXXLXGXS 31
 DB 180 SMQPEEAPARAAGAAIAGQAS 200

RESULT 26
 Q8RM05 PRELIMINARY; PRT; 631 AA.
 ID Q8RM05
 AC Q8RM05;
 DT 01-JUN-2002 (TReMBLrel. 21, Created)
 DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
 DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
 DE Sigma-54 dependent transcriptional activator.
 GN ACXR.
 OS Xanthobacter sp. (strain Py2).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Hypnomicrobacteriaceae; Xanthobacter.
 OX NCBI_TaxID=78245;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ensign S.A.;
 RC STRAIN=Py2;
 RA Sluis M.K., Larsen R.A., Krum J.G., Anderson R., Metcalf W.W.,
 RA "Biochemical, Molecular and Genetic Analyses of the Acetone
 RT Carboxylases from Xanthobacter sp. strain Py2 and Rhodobacter
 RT capsulatus strain B10."
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS A SIGMA-54 FACTOR INTERACTION ATP-BINDING
 CC DOMAIN.
 DR EMBL; AY055852; AAL17709.1; -.
 DR InterPro; IPR003593; AAA_ATPase.
 DR InterPro; IPR003018; GAF.
 DR InterPro; IPR002197; HTH_Fis.

DR InterPro: IPR002078; Sig54_interact.
 DR Pfam: PF02954; HTH_8; 1.
 DR Pfam: PF00156; Sigma54_activat; 1.
 DR SMART: SM00382; AAA; 1.
 DR SMART: SM00065; GAF; 1.
 DR TIGRfam: TIGR01199; HTH_fis; 1.
 DR PROSITE: PS00675; SIGMA54_INTERACT_1; 1.
 DR PROSITE: PS00688; SIGMA54_INTERACT_3; 1.
 DR PROSITE: PS00645; SIGMA54_INTERACT_4; 1.
 DR APP-binding: DNM-binding; Transcription regulation.
 KM APP-binding: DNM-binding; Transcription regulation.
 SQ SEQUENCE 631 AA; 68303 MW; B724DAD20D02F80C CRC64;

Query Match 33.9%; Score 38; DB 2; Length 631;
 Best Local Similarity 32.3%; Pred. No. 82;
 Matches 10; Conservative 1; Mismatches 20; Indels 0; Gaps 0;

QY 4 GTXXXXXKXEEAVRLXXXXLXGXSGA 34
 DB 582 GTAAATDLKAVEAALRAAVDACGNSRAA 612

RESULT 27

Q9UDUO PRELIMINARY; PRT; 641 AA.

AC Q9UDUO:
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAY-2003 (TrEMBLrel. 23, Last annotation update)
 DE WUSC:H.D40N23.1 protein (zinc finger sarcoma gene long A isoform)
 DE (BTB-POZ domain zinc finger transcription factor).
 GN ZSG OR R1AZ.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99063792; PubMed=9847074;
 RA Sulston J.E., Waterston R.;
 RT "toward a complete human genome sequence.";
 RL Genome Res. 8:1097-1108(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Gattung S., Geisel C., Murray J.;
 RT "The sequence of Homo sapiens PAC clone R3-400N23.";
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Waterston R.H.;
 RT Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Waterston R.;
 RT Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=2404868; PubMed=1094935;
 RA Mastrangelo T., Modena P., Tornelli S., Bullrich F., Testi A.,
 RA Mezzelani A., Radice P., Azzeletti A., Pilotti S., Croce C.;
 RA Pleiotelli M., Sozzi G.;
 RT "A novel zinc finger gene is fused to EWS in small round cell tumor.";
 RL Oncogene 19:3799-3804(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RA Chiu K.-V., Yang W.-L., Kudoh K.;
 RT "Novel CAMP Signaling Via the Regulatory Subunit of the CAMP-
 RT dependent Protein Kinase.";
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC005003; AAF01349.1;
 DR EMBL: AF254083; AAG09032.1;
 DR EMBL: AF028384; AAK19024.1;
 DR HSSP: Q05516; ICS3.
 TRANSFAC: T04797;

DR InterPro: IPR000637; AT hook.
 DR InterPro: IPR000515; BPD_transp.
 DR InterPro: IPR000210; BTB_POZ.
 DR InterPro: IPR007087; Znf_C2H2.
 DR Pfam: PF02178; AT hook; 1.
 DR Pfam: PF00651; BTB; 1.
 DR Pfam: PF00096; ZF-C2H2; 7.
 DR ProDom: PD000003; Znf_C2H2; 1.
 DR SMART: SM00384; AT hook; 1.
 DR SMART: SM00225; BTB; 1.
 DR SMART: SM00355; Znf_C2H2; 7.
 DR PROSITE: PS00402; BPD_TRANSPOIN_MEMBER; 1.
 DR PROSITE: PS00097; BTB; 1.
 DR PROSITE: PS00354; HMG1_Y; 1.
 DR PROSITE: PS00028; ZINC_FINGER_C2H2_1; 6.
 DR PROSITE: PS00157; ZINC_FINGER_C2H2_2; 6.
 DR Metal-binding; Zinc; Zinc-finger.
 SQ SEQUENCE 641 AA; 69079 MW; 29515535E380F0CE CRC64;

Query Match 33.9%; Score 38; DB 4; Length 641;
 Best Local Similarity 42.9%; Pred. No. 83;
 Matches 9; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 11 SKXEEAVRLXXXXLXGXSGS 31
 DB 205 SKQEEEAARAGAAIAGQAS 225

RESULT 28

Q9JMG9 PRELIMINARY; PRT; 641 AA.

AC Q9JMG9:
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Transcription factor MAZR.
 GN ZFP278 OR MAZR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=20136053; PubMed=10669750;
 RA Kobayashi A., Yamagawa H., Hoshino H., Muto A., Sato K., Morita M.,
 RA Hayashi N., Yamamoto M., Igatahshi K.;
 RT "A combinatorial code for gene expression generated by transcription
 RT factor bach2 and MAZR (MAZ-related factor) through the BTB/POZ
 RT domain.";
 RL Mol. Cell. Biol. 20:1733-1746(2000).
 DR EMBL: AB028397; BAA90874.1;
 DR HSSP: Q05516; ICS3.
 TRANSFAC: T04796;
 DR MGD: MGI:1691832; Zfp278.
 DR InterPro: IPR000637; AT hook.
 DR InterPro: IPR000515; BPD_transp.
 DR InterPro: IPR000210; BTB_POZ.
 DR InterPro: IPR007087; Znf_C2H2.
 DR Pfam: PF02178; AT hook; 1.
 DR Pfam: PF00651; BTB; 1.
 DR Pfam: PF00096; ZF-C2H2; 7.
 DR ProDom: PD000003; Znf_C2H2; 1.
 DR SMART: SM00384; AT hook; 1.
 DR SMART: SM00225; BTB; 1.
 DR SMART: SM00355; Znf_C2H2; 7.
 DR PROSITE: PS00402; BPD_TRANSPOIN_MEMBER; 1.
 DR PROSITE: PS00097; BTB; 1.
 DR PROSITE: PS00354; HMG1_Y; 1.
 DR PROSITE: PS00028; ZINC_FINGER_C2H2_1; 6.
 DR PROSITE: PS00157; ZINC_FINGER_C2H2_2; 6.
 DR Metal-binding; Zinc; Zinc-finger.
 SQ SEQUENCE 641 AA; 69138 MW; C4BEA972CC15A877 CRC64;

Query Match 33.9%; Score 38; DB 11; Length 641;
 Best Local Similarity 42.9%; Pred. No. 83;
 Matches 9; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 11 SKXKEEAVRLXXXXLXGXS 31
 DB 205 SMQPEEAAATCAATAGAGS 225

RESULT 29

ID Q9HBE1 PRELIMINARY; PRT; 687 AA.
 AC Q9HBE1;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Zinc finger sarcoma gene long C isoform.
 GN ZSG.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OC NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20404868; PubMed=10949935;
 RA Meistrangelo T., Modena P., Tornelli S., Bullrich F., Testi A.,
 RA Meistrangelo A., Radice P., Azzeletti A., Piloti S., Croce C.,
 RA Pierotti M., Sczzi G.;
 RT "A novel zinc finger gene is fused to EMS in small round cell tumor";
 RL Oncogene 19:3799-3804(2000).
 DR EMBL; AF254085; AAC09034.1;
 DR HSP; Q05516; ICS3.
 DR GeneW; HGNC:13071; ZNF278.
 DR InterPro; IPR000637; AT hook.
 DR InterPro; IPR000515; BFD transp.
 DR InterPro; IPR000210; BTB POZ.
 DR InterPro; IPR007087; Znf_C2H2.
 DR Pfam; PF02178; AT hook; 1.
 DR Pfam; PF00651; BTB; 1.
 DR Pfam; PF00096; Zf_C2H2; 9.
 DR Pfam; PF00003; Znf_C2H2; 1.
 DR ProDom; PD000003; Znf_C2H2; 1.
 DR SMART; SM00384; AT hook; 1.
 DR SMART; SM00225; BTB; 1.
 DR SMART; SM00355; Znf_C2H2; 9.
 DR ProSITE; PS00402; BFD_TRANS_INN_MEMBER; 1.
 DR ProSITE; PS00097; BTB; 1.
 DR ProSITE; PS00354; HMGI_Y; 1.
 DR ProSITE; PS00028; ZINC_FINGER_C2H2_1; 7.
 DR ProSITE; PS0157; ZINC_FINGER_C2H2_2; 7.
 KW Metal-binding; zinc; zinc-finger.
 SQ SEQUENCE 687 AA; 74060 MW; 0F1C59A78C6D110A CRC64;

Query Match 33.9%; Score 38; DB 4; Length 687;
 Best Local Similarity 42.9%; Pred. No. 90;
 Matches 9; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 11 SKXKEEAVRLXXXXLXGXS 31
 DB 205 SMQPEEAAATCAATAGAGS 225

RESULT 30

ID Q8XZES PRELIMINARY; PRT; 478 AA.
 AC Q8XZES;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Putative decane aldehyde dehydrogenase (BADH) oxidoreductase protein
 DE (EC 1.2.1.8).
 GN BBTB OR RSC1456 OR RS03851.
 OS Ralstonia solanacearum (Pseudomonas solanacearum).

OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Ralstoniaceae; Ralstonia.
 OC NCBI_TaxID=305;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=GM1000;
 RX MEDLINE=21681879; PubMed=11823852;
 RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
 RA Ariat M., Billault A., Brothier P., Camus J.C., Cattolico L.,
 RA Chandler M., Choise N., Claudel-Renard C., Cunac S., Demange N.,
 RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schlex T.,
 RA Siguier P., Thebaud P., Whalen M., Wincker P., Levy M.,
 RA Weissenbach J., Boucher C.A.;
 RT "Genome sequence of the plant pathogen Ralstonia solanacearum";
 RL Nature 415:497-502(2002).
 DR EMBL; AL646064; CAD15158.1;
 DR InterPro; IPR02086; Aldehyde_dehydr.
 DR Pfam; PF00171; aldehyd; 1.
 DR ProSITE; PS00070; ALDEHYDE_DEHYDR_CYS; 1.
 DR ProSITE; PS00687; ALDEHYDE_DEHYDR_GLU; 1.
 KW Oxidoreductase; Complete Proteome.
 SQ SEQUENCE 478 AA; 50375 MW; F1ADA761C20CDCA CRC64;

Query Match 33.5%; Score 37.5; DB 16; Length 478;
 Best Local Similarity 45.5%; Pred. No. 76;
 Matches 10; Conservative 2; Mismatches 7; Indels 3; Gaps 1;

QY 15 EEEAVRLXXXX--LXGXSSG 33
 DB 393 EEEAIRANDSIYGLAGVWSG 414

Search completed: December 23, 2003, 10:03:52
 Job time : 31.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 23, 2003, 10:02:47 ; Search time 25 Seconds
(without alignments)
298.814 Million cell updates/sec

Title: US-09-889-331A-48

Perfect score: 112
Sequence: 1 XXXGTXXXXXKQEEBAVRLXXXXLXGXSAGAXXXXX 40

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 696363 seqs, 186758610 residues

Total number of hits satisfying chosen parameters: 696363

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database: Published Applications_AA.*

1: /cgn2_6/prodata/1/pubppaa/US07_PUBCOMB.pep.*
2: /cgn2_6/prodata/1/pubppaa/PCT_NEW_PUB.pep.*
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4: /cgn2_6/prodata/1/pubppaa/US06_PUBCOMB.pep.*
5: /cgn2_6/prodata/1/pubppaa/US07_NEW_PUB.pep.*
6: /cgn2_6/prodata/1/pubppaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/prodata/1/pubppaa/US08_NEW_PUB.pep.*
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9: /cgn2_6/prodata/1/pubppaa/US09_PUBCOMB.pep.*
10: /cgn2_6/prodata/1/pubppaa/US09C_PUBCOMB.pep.*
11: /cgn2_6/prodata/1/pubppaa/US09C_NEW_PUB.pep.*
12: /cgn2_6/prodata/1/pubppaa/US10_PUBCOMB.pep.*
13: /cgn2_6/prodata/1/pubppaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/prodata/1/pubppaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/prodata/1/pubppaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/prodata/1/pubppaa/US10C_NEW_PUB.pep.*
17: /cgn2_6/prodata/1/pubppaa/US60_NEW_PUB.pep.*
18: /cgn2_6/prodata/1/pubppaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	70.5	62.9	36	10	US-09-003-869-171
2	70.5	62.9	36	11	US-09-756-690A-171
3	70.5	62.9	36	15	US-10-157-224A-171
4	70.5	62.9	36	15	US-10-187-051-171
5	70.5	62.9	37	10	US-09-003-869-99
6	70.5	62.9	37	10	US-09-003-869-183
7	70.5	62.9	37	11	US-09-756-690A-99
8	70.5	62.9	37	11	US-09-756-690A-183
9	70.5	62.9	37	15	US-10-157-224A-99
10	70.5	62.9	37	15	US-10-157-224A-183
11	70.5	62.9	37	15	US-10-187-051-99
12	70.5	62.9	37	15	US-10-187-051-183
13	70.5	62.9	39	10	US-09-003-869-35
14	70.5	62.9	39	10	US-09-003-869-36
15	70.5	62.9	39	10	US-09-003-869-39

16	70.5	62.9	39	11	US-09-756-690A-35	Sequence 35, Appl
17	70.5	62.9	39	11	US-09-756-690A-36	Sequence 36, Appl
18	70.5	62.9	39	11	US-09-756-690A-39	Sequence 39, Appl
19	70.5	62.9	39	15	US-10-157-224A-35	Sequence 35, Appl
20	70.5	62.9	39	15	US-10-157-224A-36	Sequence 36, Appl
21	70.5	62.9	39	15	US-10-157-224A-39	Sequence 39, Appl
22	70.5	62.9	39	15	US-10-187-051-35	Sequence 35, Appl
23	70.5	62.9	39	15	US-10-187-051-36	Sequence 36, Appl
24	70.5	62.9	39	15	US-10-187-051-39	Sequence 39, Appl
25	70.5	62.9	39	15	US-09-756-690A-11	Sequence 11, Appl
26	69.5	62.1	35	10	US-09-003-869-69	Sequence 69, Appl
27	69.5	62.1	35	10	US-09-003-869-173	Sequence 173, Appl
28	69.5	62.1	35	11	US-09-756-690A-69	Sequence 69, Appl
29	69.5	62.1	35	11	US-09-756-690A-173	Sequence 173, Appl
30	69.5	62.1	35	15	US-10-157-224A-69	Sequence 69, Appl
31	69.5	62.1	35	15	US-10-157-224A-173	Sequence 173, Appl
32	69.5	62.1	35	15	US-10-187-051-69	Sequence 69, Appl
33	69.5	62.1	35	15	US-10-187-051-173	Sequence 173, Appl
34	69.5	62.1	36	10	US-09-003-869-86	Sequence 86, Appl
35	69.5	62.1	36	10	US-09-003-869-86	Sequence 86, Appl
36	69.5	62.1	36	10	US-09-003-869-170	Sequence 170, Appl
37	69.5	62.1	36	10	US-09-003-869-184	Sequence 184, Appl
38	69.5	62.1	36	11	US-09-756-690A-67	Sequence 67, Appl
39	69.5	62.1	36	11	US-09-756-690A-86	Sequence 86, Appl
40	69.5	62.1	36	11	US-09-756-690A-170	Sequence 170, Appl
41	69.5	62.1	36	11	US-09-756-690A-184	Sequence 184, Appl
42	69.5	62.1	36	15	US-10-157-224A-67	Sequence 67, Appl
43	69.5	62.1	36	15	US-10-157-224A-86	Sequence 86, Appl
44	69.5	62.1	36	15	US-10-157-224A-170	Sequence 170, Appl
45	69.5	62.1	36	15	US-10-157-224A-184	Sequence 184, Appl
46	69.5	62.1	36	15	US-10-187-051-67	Sequence 67, Appl
47	69.5	62.1	36	15	US-10-187-051-86	Sequence 86, Appl
48	69.5	62.1	36	15	US-10-187-051-170	Sequence 170, Appl
49	69.5	62.1	36	15	US-10-187-051-184	Sequence 184, Appl
50	69.5	62.1	37	10	US-09-003-869-65	Sequence 65, Appl

ALIGNMENTS

RESULT 1
US-09-003-869-171
Sequence 171, Application US/09003869A
Patent No. US7020137666A1
GENERAL INFORMATION:
APPLICANT: BEBLEY, NIGEL ROBERT ARNOLD
APPLICANT: BEBLEY, NIGEL ROBERT ARNOLD
APPLICANT: BEBLEY, NIGEL ROBERT ARNOLD
TITLE OF INVENTION: THE REDUCTION OF FOOD INTAKE
FILE REFERENCE: 231/181
CURRENT APPLICATION NUMBER: US/09/003,869A
CURRENT FILING DATE: 1998-01-07
EARLIER APPLICATION NUMBER: US 60/034,905
EARLIER FILING DATE: 1997-01-07
EARLIER APPLICATION NUMBER: US 60/055,404
EARLIER FILING DATE: 1997-08-08
EARLIER APPLICATION NUMBER: US 60/065,442
EARLIER FILING DATE: 1997-11-14
NUMBER OF SEQ ID NOS: 188
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 171
LENGTH: 36
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: artificially synthesized sequence of novel extendin agonist
FEATURE:
NAME/KEY: AMIDATION
LOCATION: (36)...(36)

OTHER INFORMATION: amidated Pro (Prolinamide)
US-09-003-869-171

Query Match 62.9%; Score 70.5; DB 10; Length 36;
Best Local Similarity 59.4%; Pred. No. 5.8e-06;
Matches 19; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

QY 4 GTXXXXXSKQEEAVRLXXXXL-XGXSXSGA 34
DB 4 GTFTSDASKQLEEEAVRLFIEFLKXGSPSSGA 35

RESULT 2

US-09-756-690A-171
Sequence 171, Application US/09756690A
Publication No. US20030036504A1
GENERAL INFORMATION:

APPLICANT: KOLTERMAN, ORVILLE G.

APPLICANT: YOUNG, ANDREW A.

TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR MODULATION OF
TRIGLYCERIDE LEVELS AND TREATMENT OF DYSLIPIDEMIA

FILE REFERENCE: 249/124

CURRENT APPLICATION NUMBER: US/09/756,690A

PRIOR FILING DATE: 2002-04-19

PRIOR APPLICATION NUMBER: 60/175,365

PRIOR FILING DATE: 2000-01-10

NUMBER OF SEQ ID NOS: 188

SOFTWARE: PatentIn Ver 2.1

SEQ ID NO 171

LENGTH: 36

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: Description of Artificial Sequence: Exendin Agonist

OTHER INFORMATION: c-term amidation

US-09-756-690A-171

Query Match 62.9%; Score 70.5; DB 11; Length 36;
Best Local Similarity 59.4%; Pred. No. 5.8e-06;
Matches 19; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

QY 4 GTXXXXXSKQEEAVRLXXXXL-XGXSXSGA 34
DB 4 GTFTSDASKQLEEEAVRLFIEFLKXGSPSSGA 35

RESULT 3

US-10-157-224A-171
Sequence 171, Application US/10157224A
Publication No. US20030087820A1
GENERAL INFORMATION:

APPLICANT: YOUNG, ANDREW A.

APPLICANT: KOLTERMAN, ORVILLE G.

TITLE OF INVENTION: NOVEL EXENDIN AGONIST FORMULATIONS AND METHODS OF

FILE REFERENCE: 02001-050

CURRENT APPLICATION NUMBER: US/10/157,224A

PRIOR FILING DATE: 2002-05-28

PRIOR APPLICATION NUMBER: 09/889,330

PRIOR FILING DATE: 2001-07-13

PRIOR APPLICATION NUMBER: PCT/US00/00902

PRIOR FILING DATE: 2000-01-14

PRIOR APPLICATION NUMBER: 60/116,380

PRIOR FILING DATE: 1999-01-14

PRIOR APPLICATION NUMBER: 60/175,365

PRIOR FILING DATE: 2000-01-10

NUMBER OF SEQ ID NOS: 188

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 171

LENGTH: 36

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: Description of Artificial Sequence: Exendin Agonist
OTHER INFORMATION: c-term amidation
US-10-157-224A-171

Query Match 62.9%; Score 70.5; DB 15; Length 36;
Best Local Similarity 59.4%; Pred. No. 5.8e-06;
Matches 19; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

QY 4 GTXXXXXSKQEEAVRLXXXXL-XGXSXSGA 34
DB 4 GTFTSDASKQLEEEAVRLFIEFLKXGSPSSGA 35

RESULT 4

US-10-187-051-171
Sequence 171, Application US/10187051
Publication No. US20030087821A1
GENERAL INFORMATION:

APPLICANT: BEELEY, NIGEL ROBERT ARNOLD

APPLICANT: PRICKETT, KATHRYN S.

APPLICANT: BHAVSAR, SUNIL

TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR

THE REDUCTION OF FOOD INTAKE

FILE REFERENCE: 231/181

CURRENT APPLICATION NUMBER: US/10/187,051

PRIOR FILING DATE: 2002-06-28

PRIOR APPLICATION NUMBER: US/09/003,869

PRIOR FILING DATE: 1998-01-07

PRIOR APPLICATION NUMBER: US 60/034,905

PRIOR FILING DATE: 1997-01-07

PRIOR APPLICATION NUMBER: US 60/055,404

PRIOR FILING DATE: 1997-08-08

PRIOR APPLICATION NUMBER: US 60/065,442

PRIOR FILING DATE: 1997-11-14

PRIOR APPLICATION NUMBER: US 60/066,029

PRIOR FILING DATE: 1997-11-14

NUMBER OF SEQ ID NOS: 188

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 171

LENGTH: 36

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: artificially synthesized sequence of novel exendin

OTHER INFORMATION: agonist

OTHER INFORMATION: compound

FEATURE:

NAME/KEY: AMIDATION

LOCATION: (36)...

OTHER INFORMATION: amidated Pro (Prolinamide)

US-10-187-051-171

Query Match 62.9%; Score 70.5; DB 15; Length 36;
Best Local Similarity 59.4%; Pred. No. 5.8e-06;
Matches 19; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

QY 4 GTXXXXXSKQEEAVRLXXXXL-XGXSXSGA 34
DB 4 GTFTSDASKQLEEEAVRLFIEFLKXGSPSSGA 35

RESULT 5

US-09-869-99
Sequence 99, Application US/09003869A
Patent No. US2002013766A1
GENERAL INFORMATION:

APPLICANT: BEELEY, NIGEL ROBERT ARNOLD

APPLICANT: PRICKETT, KATHRYN S.

APPLICANT: BHAVSAR, SUNIL

TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR

THE REDUCTION OF FOOD INTAKE

FILE REFERENCE: 231/181
CURRENT APPLICATION NUMBER: US/09/003,869A
CURRENT FILING DATE: 1998-01-07
EARLIER APPLICATION NUMBER: US 60/034,905
EARLIER FILING DATE: 1997-01-07
EARLIER APPLICATION NUMBER: US 60/055,404
EARLIER FILING DATE: 1997-08-08
EARLIER APPLICATION NUMBER: US 60/065,442
EARLIER FILING DATE: 1997-11-14
EARLIER APPLICATION NUMBER: US 60/066,029
EARLIER FILING DATE: 1997-11-14
NUMBER OF SEQ ID NOS: 188
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 99
LENGTH: 37
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: artificially synthesized sequence of novel extendin agonist
FEATURE:
OTHER INFORMATION: compound
FEATURE:
OTHER INFORMATION: Xaa in positions 31, 36 and 37 stands for homoproline.
NAME/KEY: AMIDATION
LOCATION: (37)...(37)
OTHER INFORMATION: amidated hpro (homoprolinamide)
US-09-003-869-99
Query Match 62.9%; Score 70.5; DB 10; Length 37;
Best Local Similarity 62.5%; Pred. No. 6e-06;
Matches 20; Conservative 0; Mismatches 11; Indels 1; Gaps 1;
QY 4 GTXXXXXSKQEEAVRLXXXXL-XGXS SGA 34
DB 4 GTFTDASKQMEEAVALFIWLKNGXS SGA 35
RESULT 6
US-09-003-869-183
Sequence 183, Application US/09003869A
Patent No. US2002013766A1
GENERAL INFORMATION:
APPLICANT: BEELEY, NIGEL ROBERT ARNOLD
APPLICANT: BEELEY, KATHRYN S.
APPLICANT: BHAVSAR, SUNIL
TITLE OF INVENTION: USE OF EXTENDING AND AGONISTS THEREOF FOR
TITLE OF INVENTION: THE REDUCTION OF FOOD INTAKE
FILE REFERENCE: 231/181
CURRENT APPLICATION NUMBER: US/09/003,869A
CURRENT FILING DATE: 1998-01-07
EARLIER APPLICATION NUMBER: US 60/034,905
EARLIER FILING DATE: 1997-01-07
EARLIER APPLICATION NUMBER: US 60/055,404
EARLIER FILING DATE: 1997-08-08
EARLIER APPLICATION NUMBER: US 60/065,442
EARLIER FILING DATE: 1997-11-14
EARLIER APPLICATION NUMBER: US 60/066,029
EARLIER FILING DATE: 1997-11-14
NUMBER OF SEQ ID NOS: 188
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 183
LENGTH: 37
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: artificially synthesized sequence of novel extendin agonist
OTHER INFORMATION: compound
FEATURE:
OTHER INFORMATION: Xaa in positions 31, 36 and 37 stands for n-methylalanine.
NAME/KEY: AMIDATION
LOCATION: (37)...(37)
OTHER INFORMATION: amidated Nmeala (n-methylalaninamide)

US-09-003-869-183
Query Match 62.9%; Score 70.5; DB 10; Length 37;
Best Local Similarity 62.5%; Pred. No. 6e-06;
Matches 20; Conservative 0; Mismatches 11; Indels 1; Gaps 1;
QY 4 GTXXXXXSKQEEAVRLXXXXL-XGXS SGA 34
DB 4 GTFTSLSKQMEEAVALFIWLKNGXS SGA 35
RESULT 7
US-09-756-690A-99
Sequence 99, Application US/09756690A
Publication No. US20030036504A1
GENERAL INFORMATION:
APPLICANT: YOUNG, ANDREW A.
APPLICANT: KOLTERMAN, ORVILLE G.
TITLE OF INVENTION: USE OF EXTENDING AND AGONISTS THEREOF FOR MODULATION OF
TITLE OF INVENTION: TRIGLYCERIDE LEVELS AND TREATMENT OF DYSLIPIDEMIA
FILE REFERENCE: 249/124
CURRENT APPLICATION NUMBER: US/09/756,690A
CURRENT FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/175,365
PRIOR FILING DATE: 2000-01-10
NUMBER OF SEQ ID NOS: 188
SOFTWARE: PatentIn Ver 2.1
SEQ ID NO 99
LENGTH: 37
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Extendin Agonist
FEATURE:
NAME/KEY: MOD RES
LOCATION: (31)
OTHER INFORMATION: hpro
FEATURE:
NAME/KEY: MOD RES
LOCATION: (36)
OTHER INFORMATION: hpro
FEATURE:
NAME/KEY: MOD RES
LOCATION: (37)
OTHER INFORMATION: hpro
FEATURE:
OTHER INFORMATION: c-term amidation
US-09-756-690A-99
Query Match 62.9%; Score 70.5; DB 11; Length 37;
Best Local Similarity 62.5%; Pred. No. 6e-06;
Matches 20; Conservative 0; Mismatches 11; Indels 1; Gaps 1;
QY 4 GTXXXXXSKQEEAVRLXXXXL-XGXS SGA 34
DB 4 GTFTDASKQMEEAVALFIWLKNGXS SGA 35
RESULT 8
US-09-756-690A-183
Sequence 183, Application US/09756690A
Publication No. US20030036504A1
GENERAL INFORMATION:
APPLICANT: KOLTERMAN, ORVILLE G.
APPLICANT: YOUNG, ANDREW A.
TITLE OF INVENTION: USE OF EXTENDING AND AGONISTS THEREOF FOR MODULATION OF
TITLE OF INVENTION: TRIGLYCERIDE LEVELS AND TREATMENT OF DYSLIPIDEMIA
FILE REFERENCE: 249/124
CURRENT APPLICATION NUMBER: US/09/756,690A
CURRENT FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/175,365
PRIOR FILING DATE: 2000-01-10
NUMBER OF SEQ ID NOS: 188

SOFTWARE: PatentIn Ver 2.1
SEQ ID NO 183
LENGTH: 37
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Exendin Agonist
FEATURE:
NAME/KEY: MOD RES
LOCATION: (31)
OTHER INFORMATION: NMeala
FEATURE:
NAME/KEY: MOD RES
LOCATION: (36)
OTHER INFORMATION: NMeala
FEATURE:
NAME/KEY: MOD RES
LOCATION: (37)
OTHER INFORMATION: NMeala
FEATURE:
OTHER INFORMATION: c-term amidation
US-09-756-690A-183

Query Match 62.9%; Score 70.5; DB 11; Length 37;
Best Local Similarity 62.5%; Pred. No. 6e-06;
Matches 20; Conservative 0; Mismatches 11; Indels 1; Gaps 1;

QY 4 GTXXXXXSKOXEEAVRLXXXXL-XGXSXSGA 34
DB 4 GTFTSALSKOMEEAVRLFIEMLNKXGXSSGA 35

RESULT 9
US-10-157-224A-99
Sequence 99, Application US/10157224A
Publication No. US20030087820A1
GENERAL INFORMATION:
APPLICANT: YOUNG, ANDREW A.
TITLE OF INVENTION: NOVEL EXENDIN AGONIST FORMULATIONS AND METHODS OF
FILE REFERENCE: 02001-050
CURRENT FILING DATE: 2002-05-28
PRIOR APPLICATION NUMBER: 09/889,330
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: PCT/US00/00902
PRIOR FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: 60/116,380
PRIOR FILING DATE: 1999-01-14
PRIOR APPLICATION NUMBER: 60/175,365
PRIOR FILING DATE: 2000-01-10
NUMBER OF SEQ ID NOS: 188
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 99
LENGTH: 37
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Exendin Agonist
FEATURE:
OTHER INFORMATION: c-term amidation
FEATURE:
NAME/KEY: MOD RES
LOCATION: (31)
OTHER INFORMATION: Homoproline
FEATURE:
NAME/KEY: MOD RES
LOCATION: (36)
OTHER INFORMATION: Homoproline
US-10-157-224A-99

Query Match 62.9%; Score 70.5; DB 15; Length 37;

Best Local Similarity 62.5%; Pred. No. 6e-06;
Matches 20; Conservative 0; Mismatches 11; Indels 1; Gaps 1;

QY 4 GTXXXXXSKOXEEAVRLXXXXL-XGXSXSGA 34
DB 4 GTFTSDASKOMEEAVRLFIEMLNKXGXSSGA 35

RESULT 10
US-10-157-224A-183
Sequence 183, Application US/10157224A
Publication No. US20030087820A1
GENERAL INFORMATION:
APPLICANT: YOUNG, ANDREW A.
TITLE OF INVENTION: NOVEL EXENDIN AGONIST FORMULATIONS AND METHODS OF
FILE REFERENCE: 02001-050
CURRENT FILING DATE: 2002-05-28
PRIOR APPLICATION NUMBER: US/10/157,224A
CURRENT FILING DATE: 2002-05-28
PRIOR APPLICATION NUMBER: 09/889,330
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: PCT/US00/00902
PRIOR FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: 60/116,380
PRIOR FILING DATE: 1999-01-14
PRIOR APPLICATION NUMBER: 60/175,365
PRIOR FILING DATE: 2000-01-10
NUMBER OF SEQ ID NOS: 188
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 183
LENGTH: 37
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Exendin Agonist
FEATURE:
OTHER INFORMATION: c-term amidation
FEATURE:
NAME/KEY: MOD RES
LOCATION: (31)
OTHER INFORMATION: N-methylalanine
FEATURE:
NAME/KEY: MOD RES
LOCATION: (36)
OTHER INFORMATION: N-methylalanine
US-10-157-224A-183

Query Match 62.9%; Score 70.5; DB 15; Length 37;
Best Local Similarity 62.5%; Pred. No. 6e-06;
Matches 20; Conservative 0; Mismatches 11; Indels 1; Gaps 1;

QY 4 GTXXXXXSKOXEEAVRLXXXXL-XGXSXSGA 34
DB 4 GTFTSALSKOMEEAVRLFIEMLNKXGXSSGA 35

RESULT 11
US-10-187-051-99
Sequence 99, Application US/10187051
Publication No. US20030087821A1
GENERAL INFORMATION:
APPLICANT: BEELEY, NIGEL ROBERT ARNOLD
APPLICANT: PRICKETT, KATHRYN S.
APPLICANT: BHAVSAR, SUNIL
TITLE OF INVENTION: USE OF EXENDIN AND AGONISTS THEREOF FOR
FILE REFERENCE: 231/181
CURRENT FILING DATE: US/10/187,051
CURRENT FILING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: US/09/003,869
PRIOR FILING DATE: 1998-01-07
PRIOR APPLICATION NUMBER: US 60/034,905

PRIOR FILING DATE: 1997-01-07
PRIOR APPLICATION NUMBER: US 60/055,404
PRIOR FILING DATE: 1997-08-08
PRIOR APPLICATION NUMBER: US 60/065,442
PRIOR FILING DATE: 1997-11-14
PRIOR APPLICATION NUMBER: US 60/066,029
PRIOR FILING DATE: 1997-11-14
NUMBER OF SEQ ID NOS: 188
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 99
LENGTH: 37
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: artificially synthesized sequence of novel extendin
OTHER INFORMATION: agonist
OTHER INFORMATION: compound
FEATURE:
OTHER INFORMATION: Xaa in positions 31, 36 and 37 stands for homoproline.
NAME/KEY: AMIDATION
LOCATION: (37)...(37)
OTHER INFORMATION: amidated hPro (homoprolinamide)
US-10-187-051-99

Query Match
Best Local Similarity 62.5%; Score 70.5; DB 15; Length 37;
Best Local Similarity 62.5%; Pred. No. 6e-06; Mismatches 11; Indels 1; Gaps 1;
Matches 20; Conservative 0; Mismatches 11; Indels 1; Gaps 1;

QY 4 GTXXXXXSKQEEAVRLXXXXL-XGXSXSGA 34
DB 4 GTFTSDLSKQEEAVRLFTFLKNGXSXSGA 35

RESULT 12
US-10-187-051-183
Sequence 183, Application US/10187051
Publication No. US20030087821A1
GENERAL INFORMATION:
APPLICANT: BEELEY, NIGEL ROBERT ARNOLD
APPLICANT: PRICKETT, KATHRYN S.
APPLICANT: BHAVSAR, SUNIL
TITLE OF INVENTION: USE OF EXTENDIN AND AGONISTS THEREOF FOR
FILE REFERENCE: 231/181
CURRENT APPLICATION NUMBER: US/10/187,051
CURRENT FILING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: US/09/003,869
PRIOR FILING DATE: 1998-01-07
PRIOR APPLICATION NUMBER: US 60/034,905
PRIOR FILING DATE: 1997-01-07
PRIOR APPLICATION NUMBER: US 60/055,404
PRIOR FILING DATE: 1997-08-08
PRIOR APPLICATION NUMBER: US 60/065,442
PRIOR FILING DATE: 1997-11-14
PRIOR APPLICATION NUMBER: US 60/066,029
PRIOR FILING DATE: 1997-11-14
NUMBER OF SEQ ID NOS: 188
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 183
LENGTH: 37
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: artificially synthesized sequence of novel extendin
OTHER INFORMATION: agonist
OTHER INFORMATION: compound
FEATURE:
OTHER INFORMATION: Xaa in positions 31, 36 and 37 stands for n-
OTHER INFORMATION: methylaniline.
NAME/KEY: AMIDATION
LOCATION: (37)...(37)

OTHER INFORMATION: amidated Nmeala (n-methylanilineamide)
US-10-187-051-183

Query Match
Best Local Similarity 62.5%; Score 70.5; DB 15; Length 37;
Best Local Similarity 62.5%; Pred. No. 6e-06; Mismatches 11; Indels 1; Gaps 1;
Matches 20; Conservative 0; Mismatches 11; Indels 1; Gaps 1;

QY 4 GTXXXXXSKQEEAVRLXXXXL-XGXSXSGA 34
DB 4 GTFTSDLSKQEEAVRLFTFLKNGXSXSGA 35

RESULT 13
US-09-003-869-35
Sequence 35, Application US/09003869A
Patent No. US20020137666A1
GENERAL INFORMATION:
APPLICANT: BEELEY, NIGEL ROBERT ARNOLD
APPLICANT: PRICKETT, KATHRYN S.
APPLICANT: BHAVSAR, SUNIL
TITLE OF INVENTION: USE OF EXTENDIN AND AGONISTS THEREOF FOR
FILE REFERENCE: 231/181
CURRENT APPLICATION NUMBER: US/09/003,869A
CURRENT FILING DATE: 1998-01-07
EARLIER APPLICATION NUMBER: US 60/034,905
EARLIER FILING DATE: 1997-01-07
EARLIER APPLICATION NUMBER: US 60/055,404
EARLIER FILING DATE: 1997-08-08
EARLIER APPLICATION NUMBER: US 60/065,442
EARLIER FILING DATE: 1997-11-14
EARLIER APPLICATION NUMBER: US 60/066,029
EARLIER FILING DATE: 1997-11-14
NUMBER OF SEQ ID NOS: 188
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 35
LENGTH: 39
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: artificially synthesized sequence of novel extendin agonist
OTHER INFORMATION: compound
FEATURE:
OTHER INFORMATION: Xaa in positions 31, 36, 37 and 38 stands for thioproline.
NAME/KEY: AMIDATION
LOCATION: (39)...(39)
OTHER INFORMATION: amidated Ser (Serinamide)
US-09-003-869-35

Query Match
Best Local Similarity 62.5%; Score 70.5; DB 10; Length 39;
Best Local Similarity 62.5%; Pred. No. 6.3e-06; Mismatches 11; Indels 1; Gaps 1;
Matches 20; Conservative 0; Mismatches 11; Indels 1; Gaps 1;

QY 4 GTXXXXXSKQEEAVRLXXXXL-XGXSXSGA 34
DB 4 GTFTSDLSKQEEAVRLFTFLKNGXSXSGA 35

RESULT 14
US-09-003-869-36
Sequence 36, Application US/09003869A
Patent No. US20020137666A1
GENERAL INFORMATION:
APPLICANT: BEELEY, NIGEL ROBERT ARNOLD
APPLICANT: PRICKETT, KATHRYN S.
APPLICANT: BHAVSAR, SUNIL
TITLE OF INVENTION: USE OF EXTENDIN AND AGONISTS THEREOF FOR
FILE REFERENCE: 231/181
CURRENT APPLICATION NUMBER: US/09/003,869A
CURRENT FILING DATE: 1998-01-07
EARLIER APPLICATION NUMBER: US 60/034,905

EARLIER FILING DATE: 1997-01-07
EARLIER APPLICATION NUMBER: US 60/055,404
EARLIER FILING DATE: 1997-08-08
EARLIER APPLICATION NUMBER: US 60/065,442
EARLIER FILING DATE: 1997-11-14
EARLIER APPLICATION NUMBER: US 60/066,029
EARLIER FILING DATE: 1997-11-14
NUMBER OF SEQ ID NOS: 188
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 36
LENGTH: 39
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: artificially synthesized sequence of novel extendin agonist
OTHER INFORMATION: compound
FEATURE:
OTHER INFORMATION: Xaa in positions 31, 36, 37 and 38 stands for homoproline.
FEATURE:
NAME/KEY: AMIDATION
LOCATION: (39)...(39)
OTHER INFORMATION: amidated Ser (Serinamide)
US-09-003-869-36

Query Match 62.9%; Score 70.5; DB 10; Length 39;
Best Local Similarity 62.5%; Pred. No. 6.3e-06;
Matches 20; Conservative 0; Mismatches 11; Indels 1; Gaps 1;

QY 4 GTXXXXXSKQXEEAVRLXXXXL-XGXS SGA 34
DB 4 GTFTSDLSKQLEEEAVRLFIEFLKNGXS SGA 35

RESULT 15
US-09-003-869-39
Sequence 39, Application US/09003869A
Patent No. US20020137666A1
GENERAL INFORMATION:
APPLICANT: BEILEY, NIGEL ROBERT ARNOLD
APPLICANT: BRACKETT, KATHRYN S.
APPLICANT: BHAVSAR, SUNIL
TITLE OF INVENTION: USE OF EXTENDINS AND AGONISTS THEREOF FOR
FILE REFERENCE: 231/181
CURRENT APPLICATION NUMBER: US/09/003,869A
CURRENT FILING DATE: 1998-01-07
EARLIER APPLICATION NUMBER: US 60/034,905
EARLIER FILING DATE: 1997-01-07
EARLIER APPLICATION NUMBER: US 60/055,404
EARLIER FILING DATE: 1997-08-08
EARLIER APPLICATION NUMBER: US 60/065,442
EARLIER FILING DATE: 1997-11-14
EARLIER APPLICATION NUMBER: US 60/066,029
EARLIER FILING DATE: 1997-11-14
NUMBER OF SEQ ID NOS: 188
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 39
LENGTH: 39
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: artificially synthesized sequence of novel extendin agonist
OTHER INFORMATION: compound
FEATURE:
OTHER INFORMATION: Xaa in positions 31, 36, 37 and 38 stands for n-methylalanine.
NAME/KEY: AMIDATION
LOCATION: (39)...(39)
OTHER INFORMATION: amidated Ser (Serinamide)
US-09-003-869-39

Query Match 62.9%; Score 70.5; DB 10; Length 39;
Best Local Similarity 62.5%; Pred. No. 6.3e-06;

Matches 20; Conservative 0; Mismatches 11; Indels 1; Gaps 1;

QY 4 GTXXXXXSKQXEEAVRLXXXXL-XGXS SGA 34
DB 4 GTFTSDLSKQLEEEAVRLFIEFLKNGXS SGA 35

RESULT 16
US-09-756-690A-35
Sequence 35, Application US/09756690A
Publication No. US20030036504A1
GENERAL INFORMATION:
APPLICANT: KOLTERMAN, ORVILLE G.
APPLICANT: YOUNG, ANDREW A.
TITLE OF INVENTION: USE OF EXTENDINS AND AGONISTS THEREOF FOR MODULATION OF
TRIGLYCERIDE LEVELS AND TREATMENT OF DYSLIPIDEMIA
FILE REFERENCE: 249/124
CURRENT APPLICATION NUMBER: US/09/756,690A
CURRENT FILING DATE: 2002-04-19
PRIOR FILING DATE: 2000-01-10
NUMBER OF SEQ ID NOS: 188
SOFTWARE: Patentln Ver 2.1
SEQ ID NO 35
LENGTH: 39
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Extendin Agonist
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (31)
OTHER INFORMATION: tPro
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (36)
OTHER INFORMATION: tPro
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (38)
OTHER INFORMATION: tPro
FEATURE:
OTHER INFORMATION: c-term amidation
US-09-756-690A-35

Query Match 62.9%; Score 70.5; DB 11; Length 39;
Best Local Similarity 62.5%; Pred. No. 6.3e-06;
Matches 20; Conservative 0; Mismatches 11; Indels 1; Gaps 1;

QY 4 GTXXXXXSKQXEEAVRLXXXXL-XGXS SGA 34
DB 4 GTFTSDLSKQLEEEAVRLFIEFLKNGXS SGA 35

RESULT 17
US-09-756-690A-36
Sequence 36, Application US/09756690A
Publication No. US20030036504A1
GENERAL INFORMATION:
APPLICANT: KOLTERMAN, ORVILLE G.
APPLICANT: YOUNG, ANDREW A.
TITLE OF INVENTION: USE OF EXTENDINS AND AGONISTS THEREOF FOR MODULATION OF
TRIGLYCERIDE LEVELS AND TREATMENT OF DYSLIPIDEMIA
FILE REFERENCE: 249/124
CURRENT APPLICATION NUMBER: US/09/756,690A
CURRENT FILING DATE: 2002-04-19
PRIOR FILING DATE: 2000-01-10
NUMBER OF SEQ ID NOS: 188

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; OTHER INFORMATION: MEALA
; FEATURE:
; OTHER INFORMATION: c-term amidation
US-09-756-690A-39

Query Match      62.9%; Score 70.5; DB 11; Length 39;
Best Local Similarity 62.5%; Pred. No. 6,3e-06;
Matches 20; Conservative 0; Mismatches 11; Indels 1; Gaps 1.

Oy      4 GTXXXXXSKXEEAVRLXXXXL-XGGXSSGA 34
         |||||
Db      4 GTFTSDLSKQLEBEAVRLFIEFLNKGXSSGA 35

RESULT 19
US-10-157-224A-35
; Sequence 35, Application US/10157224A
; Publication No. US20030087820A1
; GENERAL INFORMATION:
; APPLICANT: YOUNG, ANDREW A.
; APPLICANT: KOTTERMAN, CRVILLE G.
; TITLE OF INVENTION: NOVEL EXTENDIN AGONIST FORMULATIONS AND METHODS OF
; FILE REFERENCE: 02001-050
CURRENT FILING DATE: 2002-05-28
CURRENT APPLICATION NUMBER: US/10/157,224A
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: PCT/US00/00902
PRIOR FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: 60/116,380
PRIOR FILING DATE: 1999-01-14
PRIOR APPLICATION NUMBER: 60/1175,365
PRIOR FILING DATE: 2000-01-10
NUMBER OF SEQ ID NOS: 188
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 35
LENGTH: 39
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Extendin Agonist
FEATURE:
OTHER INFORMATION: c-term amidation
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (31)
OTHER INFORMATION: thiotroline
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (36)..(38)
OTHER INFORMATION: thiotroline
US-10-157-224A-35

Query Match      62.9%; Score 70.5; DB 15; Length 39;
Best Local Similarity 62.5%; Pred. No. 6,3e-06;
Matches 20; Conservative 0; Mismatches 11; Indels 1; Gaps 1.

Oy      4 GTXXXXXSKXEEAVRLXXXXL-XGGXSSGA 34
         |||||
Db      4 GTFTSDLSKQLEBEAVRLFIEFLNKGXSSGA 35

RESULT 20
US-10-157-224A-36
; Sequence 36, Application US/10157224A
; Publication No. US20030087820A1
; GENERAL INFORMATION:
; APPLICANT: YOUNG, ANDREW A.
; APPLICANT: KOTTERMAN, CRVILLE G.
; TITLE OF INVENTION: NOVEL EXTENDIN AGONIST FORMULATIONS AND METHODS OF
; FILE REFERENCE: 02001-050

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CURRENT APPLICATION NUMBER: US/10/157,224A
CURRENT FILING DATE: 2002-05-28
PRIOR APPLICATION NUMBER: 09/889,330
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: PCT/US00/00902
PRIOR FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: 60/116,380
PRIOR FILING DATE: 1999-01-14
PRIOR APPLICATION NUMBER: 60/175,365
PRIOR FILING DATE: 2000-01-10
NUMBER OF SEQ ID NOS: 188
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 36
LENGTH: 39
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE: Description of Artificial Sequence: Exendin Agonist
OTHER INFORMATION: c-term amidation
FEATURE: NAME/KEY: MOD RES
LOCATION: (31)
OTHER INFORMATION: homoproline
FEATURE: NAME/KEY: MOD RES
LOCATION: (36)...(38)
OTHER INFORMATION: homoproline
US-10-157-224A-36

Query Match
Best Local Similarity 62.9%; Score 70.5; DB 15; Length 39;
Matches 20; Conservative 0; Mismatches 11; Indels 1; Gaps 1;

Qy 4 GTXXXXXSKQEEBAAVRLXXXXL-XGXSXSGA 34
Db 4 GTFTSDLSKQLEBAAVRLFIETLKNXGXSXSGA 35

RESULT 21
US-10-157-224A-39
Sequence 39, Application US/10157224A
Publication No. US20030087820A1
GENERAL INFORMATION:
APPLICANT: YOUNG, ANDREW A.
TITLE OF INVENTION: NOVEL EXENDIN AGONIST FORMULATIONS AND METHODS OF
FILE REFERENCE: 02001-050
CURRENT APPLICATION NUMBER: US/10/157,224A
CURRENT FILING DATE: 2002-05-28
PRIOR APPLICATION NUMBER: 09/889,330
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: PCT/US00/00902
PRIOR FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: 60/116,380
PRIOR FILING DATE: 1999-01-14
PRIOR APPLICATION NUMBER: 60/175,365
PRIOR FILING DATE: 2000-01-10
NUMBER OF SEQ ID NOS: 188
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 39
LENGTH: 39
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE: Description of Artificial Sequence: Exendin Agonist
OTHER INFORMATION: c-term amidation
FEATURE: NAME/KEY: MOD RES
LOCATION: (31)
OTHER INFORMATION: N-methylalanine

FEATURE:
NAME/KEY: MOD RES
LOCATION: (36)...(38)
OTHER INFORMATION: N-methylalanine
US-10-157-224A-39

Query Match
Best Local Similarity 62.9%; Score 70.5; DB 15; Length 39;
Matches 20; Conservative 0; Mismatches 11; Indels 1; Gaps 1;

Qy 4 GTXXXXXSKQEEBAAVRLXXXXL-XGXSXSGA 34
Db 4 GTFTSDLSKQLEBAAVRLFIETLKNXGXSXSGA 35

RESULT 22
US-10-187-051-35
Sequence 35, Application US/10187051
Publication No. US20030087821A1
GENERAL INFORMATION:
APPLICANT: BEELEY, NIGEL ROBERT ARNOLD
APPLICANT: PRICKETT, KATHRYN S.
APPLICANT: BHAVSAR, SONIL
TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR
FILE REFERENCE: 231/181
CURRENT APPLICATION NUMBER: US/10/187,051
CURRENT FILING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: US/09/003,869
PRIOR FILING DATE: 1998-01-07
PRIOR APPLICATION NUMBER: US 60/034,905
PRIOR FILING DATE: 1997-01-07
PRIOR APPLICATION NUMBER: US 60/055,404
PRIOR FILING DATE: 1997-08-08
PRIOR APPLICATION NUMBER: US 60/065,442
PRIOR FILING DATE: 1997-11-14
PRIOR APPLICATION NUMBER: US 60/066,029
PRIOR FILING DATE: 1997-11-14
NUMBER OF SEQ ID NOS: 188
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 35
LENGTH: 39
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE: artificially synthesized sequence of novel exendin
OTHER INFORMATION: agonist
OTHER INFORMATION: compound
FEATURE: OTHER INFORMATION: Xaa in positions 31, 36, 37 and 38 stands for
OTHER INFORMATION: thioisoproline.
FEATURE: NAME/KEY: AMIDATION
LOCATION: (39)...(39)
OTHER INFORMATION: amidated Ser (Serinamide)
US-10-187-051-35

Query Match
Best Local Similarity 62.9%; Score 70.5; DB 15; Length 39;
Matches 20; Conservative 0; Mismatches 11; Indels 1; Gaps 1;

Qy 4 GTXXXXXSKQEEBAAVRLXXXXL-XGXSXSGA 34
Db 4 GTFTSDLSKQLEBAAVRLFIETLKNXGXSXSGA 35

RESULT 23
US-10-187-051-36
Sequence 36, Application US/10187051
Publication No. US20030087821A1
GENERAL INFORMATION:
APPLICANT: BEELEY, NIGEL ROBERT ARNOLD
APPLICANT: PRICKETT, KATHRYN S.

APPLICANT: BHAVSAR, SUNIL
TITLE OF INVENTION: USE OF EXTENDING AND AGONISTS THEREOF FOR
FILE REFERENCE: 231/181
CURRENT APPLICATION NUMBER: US/10/187,051
CURRENT FILING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: US/09/003,869
PRIOR FILING DATE: 1998-01-07
PRIOR APPLICATION NUMBER: US 60/034,905
PRIOR FILING DATE: 1997-01-07
PRIOR APPLICATION NUMBER: US 60/055,404
PRIOR FILING DATE: 1997-08-08
PRIOR APPLICATION NUMBER: US 60/065,442
PRIOR FILING DATE: 1997-11-14
PRIOR APPLICATION NUMBER: US 60/066,029
PRIOR FILING DATE: 1997-11-14
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 36
LENGTH: 39
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: artificially synthesized sequence of novel extendin
OTHER INFORMATION: agonist
OTHER INFORMATION: compound
FEATURE:
OTHER INFORMATION: Xaa in positions 31, 36, 37 and 38 stands for
OTHER INFORMATION: homoproline.
FEATURE:
NAME/KEY: AMIDATION
LOCATION: (39)...(39)
OTHER INFORMATION: amidated Ser (Serinamide)
US-10-187-051-36

Query Match 62.9%; Score 70.5; DB 15; Length 39;
Best Local Similarity 62.5%; Pred. No. 6.3e-06;
Matches 20; Conservative 0; Mismatches 11; Indels 1; Gaps 1;

Qy 4 GTXXXXXSKQEEAVRLXXXXL-XGXSSGA 34
Db 4 GTFTSDLSKQLEEAVALFIEFLKNGXSSGA 35

RESULT 24
US-10-187-051-39
Sequence 39, Application US/10.87051
Publication No. US20030087821A1
GENERAL INFORMATION:
APPLICANT: BEELEY, NIGEL ROBERT ARNOLD
APPLICANT: PRICKETT, KATHRYN S.
APPLICANT: BHAVSAR, SUNIL
TITLE OF INVENTION: USE OF EXTENDING AND AGONISTS THEREOF FOR
FILE REFERENCE: 231/181
CURRENT APPLICATION NUMBER: US/10/187,051
CURRENT FILING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: US/09/003,869
PRIOR FILING DATE: 1998-01-07
PRIOR APPLICATION NUMBER: US 60/034,905
PRIOR FILING DATE: 1997-01-07
PRIOR APPLICATION NUMBER: US 60/055,404
PRIOR FILING DATE: 1997-08-08
PRIOR APPLICATION NUMBER: US 60/065,442
PRIOR FILING DATE: 1997-11-14
PRIOR APPLICATION NUMBER: US 60/066,029
PRIOR FILING DATE: 1997-11-14
NUMBER OF SEQ ID NOS: 188
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 39
LENGTH: 39
TYPE: PRT
ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: artificially synthesized sequence of novel extendin
OTHER INFORMATION: agonist
OTHER INFORMATION: compound
FEATURE:
OTHER INFORMATION: Xaa in positions 31, 36, 37 and 38 stands for n-
OTHER INFORMATION: methyllalanine.
FEATURE:
NAME/KEY: AMIDATION
LOCATION: (39)...(39)
OTHER INFORMATION: amidated Ser (Serinamide)
US-10-187-051-39

Query Match 62.9%; Score 70.5; DB 15; Length 39;
Best Local Similarity 62.5%; Pred. No. 6.3e-06;
Matches 20; Conservative 0; Mismatches 11; Indels 1; Gaps 1;

Qy 4 GTXXXXXSKQEEAVRLXXXXL-XGXSSGA 34
Db 4 GTFTSDLSKQLEEAVALFIEFLKNGXSSGA 35

RESULT 25
US-09-756-690A-11
Sequence 11, Application US/09756690A
Publication No. US20030036504A1
GENERAL INFORMATION:
APPLICANT: YOUNG, ANDREW A.
APPLICANT: KOLTERMAN, ORVILLE G.
TITLE OF INVENTION: USE OF EXTENDING AND AGONISTS THEREOF FOR MODULATION OF
TITLE OF INVENTION: TRIGLYCERIDE LEVELS AND TREATMENT OF DYSLIPIDEMIA
FILE REFERENCE: 249/124
CURRENT APPLICATION NUMBER: US/09/756,690A
CURRENT FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/175,365
PRIOR FILING DATE: 2000-01-10
NUMBER OF SEQ ID NOS: 188
SOFTWARE: PatentIn Ver 2.1
SEQ ID NO 11
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Extendin Agonist
OTHER INFORMATION: c-term amidation
US-09-756-690A-11

Query Match 62.5%; Score 70; DB 11; Length 38;
Best Local Similarity 54.8%; Pred. No. 7.6e-06;
Matches 17; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 4 GTXXXXXSKQEEAVRLXXXXL-XGXSSGA 34
Db 4 GTFTSDLSKQLEEAVALFIEFLKNGXSSGA 34

RESULT 26
US-09-003-869-69
Sequence 69, Application US/09003869A
Patent No. US20020137666A1
GENERAL INFORMATION:
APPLICANT: BEELEY, NIGEL ROBERT ARNOLD
APPLICANT: PRICKETT, KATHRYN S.
APPLICANT: BHAVSAR, SUNIL
TITLE OF INVENTION: USE OF EXTENDING AND AGONISTS THEREOF FOR
FILE REFERENCE: 231/181
CURRENT APPLICATION NUMBER: US/09/003,869A
CURRENT FILING DATE: 1998-01-07
EARLIER APPLICATION NUMBER: US 60/034,905
EARLIER FILING DATE: 1997-01-07
EARLIER APPLICATION NUMBER: US 60/055,404

EARLIER FILING DATE: 1997-08-08
; EARLIER APPLICATION NUMBER: US 60/065,442
; EARLIER FILING DATE: 1997-11-14
; EARLIER APPLICATION NUMBER: US 60/066,029
; EARLIER FILING DATE: 1997-11-14
; NUMBER OF SEQ ID NOS: 188
; SOFTWARE: fastseq for Windows Version 3.0
; SEQ ID NO 69
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: artificially synthesized sequence of novel extendin agonist
; OTHER INFORMATION: compound
; FEATURE:
; NAME/KEY: AMIDATION
; LOCATION: (35)...(35)
; OTHER INFORMATION: amidated Ala (Alaninamide)
US-09-003-869-69

Query Match 62.1%; Score 69.5; DB 10; Length 35;
Best Local Similarity 59.4%; Pred. No. 8.6e-06;
Matches 19; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

QY 4 GTXXXXXKQXEEAVRLXXXXL-XGXSSGA 34
DB 4 GTFTSDLSKQLEEEAVRLFIEFLKNGGPPSSGA 35

RESULT 27
US-09-003-869-173
; Sequence 173; Application US/09003869A
; Patent No. US2002013766A1
; GENERAL INFORMATION:
; APPLICANT: BEELEY, NIGEL, ROBERT ARNOLD
; APPLICANT: BRICKETT, KATHRYN S.
; APPLICANT: BHAVSAR, SONIL
; TITLE OF INVENTION: USE OF EXTENDIN AND AGONISTS THEREOF FOR
; FILE REFERENCE: 231/181
; CURRENT APPLICATION NUMBER: US/09/003,869A
; CURRENT FILING DATE: 1998-01-07
; EARLIER APPLICATION NUMBER: US 60/034,905
; EARLIER FILING DATE: 1997-01-07
; EARLIER APPLICATION NUMBER: US 60/055,404
; EARLIER FILING DATE: 1997-08-08
; EARLIER APPLICATION NUMBER: US 60/065,442
; EARLIER FILING DATE: 1997-11-14
; EARLIER APPLICATION NUMBER: US 60/066,029
; EARLIER FILING DATE: 1997-11-14
; NUMBER OF SEQ ID NOS: 188
; SOFTWARE: fastseq for Windows Version 3.0
; SEQ ID NO 173
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: artificially synthesized sequence of novel extendin agonist
; OTHER INFORMATION: compound
; FEATURE:
; NAME/KEY: AMIDATION
; LOCATION: (35)...(35)
; OTHER INFORMATION: amidated Ala (Alaninamide)
US-09-003-869-173

Query Match 62.1%; Score 69.5; DB 10; Length 35;
Best Local Similarity 59.4%; Pred. No. 8.6e-06;
Matches 19; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

QY 4 GTXXXXXKQXEEAVRLXXXXL-XGXSSGA 34
DB 4 GTFTSDLSKQLEEEAVRLFIEFLKNGGPPSSGA 35

RESULT 28
US-09-756-690A-69
; Sequence 69; Application US/09756690A
; Publication No. US20030036504A1
; GENERAL INFORMATION:
; APPLICANT: KOTLERMAN, ORVILLE G.
; APPLICANT: YOUNG, ANDREW A.
; TITLE OF INVENTION: USE OF EXTENDIN AND AGONISTS THEREOF FOR MODULATION OF
; FILE REFERENCE: 249/124
; CURRENT APPLICATION NUMBER: US/09/756,690A
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/175,365
; PRIOR FILING DATE: 2000-01-10
; NUMBER OF SEQ ID NOS: 188
; SOFTWARE: PatentIn Ver 2.1
; SEQ ID NO 69
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Extendin Agonist
; OTHER INFORMATION: c-term amidation
US-09-756-690A-69

Query Match 62.1%; Score 69.5; DB 11; Length 35;
Best Local Similarity 59.4%; Pred. No. 8.6e-06;
Matches 19; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

QY 4 GTXXXXXKQXEEAVRLXXXXL-XGXSSGA 34
DB 4 GTFTSDLSKQLEEEAVRLFIEFLKNGGPPSSGA 35

RESULT 29
US-09-756-690A-173
; Sequence 173; Application US/09756690A
; Publication No. US20030036504A1
; GENERAL INFORMATION:
; APPLICANT: YOUNG, ANDREW A.
; APPLICANT: KOTLERMAN, ORVILLE G.
; TITLE OF INVENTION: USE OF EXTENDIN AND AGONISTS THEREOF FOR MODULATION OF
; FILE REFERENCE: 249/124
; CURRENT APPLICATION NUMBER: US/09/756,690A
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/175,365
; PRIOR FILING DATE: 2000-01-10
; NUMBER OF SEQ ID NOS: 188
; SOFTWARE: PatentIn Ver 2.1
; SEQ ID NO 173
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Extendin Agonist
; OTHER INFORMATION: c-term amidation
US-09-756-690A-173

Query Match 62.1%; Score 69.5; DB 11; Length 35;
Best Local Similarity 59.4%; Pred. No. 8.6e-06;
Matches 19; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

QY 4 GTXXXXXKQXEEAVRLXXXXL-XGXSSGA 34
DB 4 GTFTSDLSKQLEEEAVRLFIEFLKNGGPPSSGA 35

RESULT 30
US-10-157-224A-69

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: Sequence 69, Application US/10157224A
: Publication No. US20030087820A1
: GENERAL INFORMATION:
: APPLICANT: YOUNG, ANDREW A.
: APPLICANT: KOLTERMAN, ORVILLE G.
: TITLE OF INVENTION: NOVEL EXENDIN AGONIST FORMULATIONS AND METHODS OF
: FILE REFERENCE: 02001-050
: ADMINISTRATION THEREOF
: CURRENT APPLICATION NUMBER: US/10/157,224A
: CURRENT FILING DATE: 2002-05-28
: PRIOR APPLICATION NUMBER: 09/889,330
: PRIOR FILING DATE: 2001-07-13
: PRIOR APPLICATION NUMBER: PCT/US00/00902
: PRIOR FILING DATE: 2000-01-14
: PRIOR APPLICATION NUMBER: 60/116,380
: PRIOR FILING DATE: 1999-01-14
: PRIOR APPLICATION NUMBER: 60/175,365
: PRIOR FILING DATE: 2000-01-10
: NUMBER OF SEQ ID NOS: 188
: SOFTWARE: Patent Ver. 2.1
: SEQ ID NO: 69
: LENGTH: 35
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Exendin Agonist
: OTHER INFORMATION: c-term amidation
US-10-157-224A-69

Query Match      62.1%; Score 69.5; DB 15; Length 35;
Best Local Similarity 59.4%; Pred. No. 8.6e-06;
Matches 19; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

QY      4 GTXXXXXSKQEEEAVALXXXXL-XGXSXSGA 34
         |||||
DB      4 GTFTSDLSKQLEEAVALFIETLXNGGPRSSGA 35

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Search completed: December 23, 2003, 10:12:01
 Job time : 25.5 secs